From:

Slobodyansky, Elizabeth

Sent:

Tuesday, August 22, 2006 6:23 PM

To: Subject: STIC-Biotech/ChemLib 10665715 seq

Please search for case 10/665,715:

SEQ ID NO: 16 against commercial and interference databases.

Thank you.

Elizabeth Slobodyansky, PhD

**Primary Examiner** Art Unit 1652 **REM 2D83** 571-272-0941 MAILBOX 2C70

9.65

\*\*\*\*\*\*\* Searcher:\_ Searcher Phone:\_ Date Searcher Picked up: Date completed: \$-\square Searcher Prep Time:\_ Online Time:\_

Type of Search AA#: Oligomer: S/L:\_ Encode/Transl:\_ Structure #:\_\_\_ \_Text:\_ Inventor:\_\_\_ \_\_ Litigation:\_

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\*\*\*\*\*\*\* Vendors and cost where applicable STN: DIALOG: QUESTEL/ORBIT: LEXIS/NEXIS: SEQUENCE SYSTEM:\_ WWW/Internet:\_ Other (Specify):

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

August 25, 2006, 07:13:17; Search time 194 Seconds (without alignments) 1277.378 Million cell updates/sec ë :

Run

US-10-665-715-16 2879

542 1 MEPDSVIEDKTIELMCSVPR......ppsaqnetrspsrtytysr Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 2589679 segs, 457216429 residues Searched:

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seq length: 0 seq length: 200000000 Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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geneseqp1980s:\* geneseqp1990s:\* geneseqp2001s:\* geneseqp2001s:\* geneseqp2003ss:\* geneseqp2003bs:\* geneseqp2003bs:\* geneseqp2006s:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		*				
Result No.	t Score	Query Match	Length	DB	ID	Description
. '	1 2879	100.0	542	6	AAY96696	Aay96696 Human E3
••	2 2879	100.0	542	4	AAM79127	Aam79127 Human pro
•	3 2879	100.0	542	4	AAM40208	Aam40208 Human pol
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•	7 2873	99.8	542	σ	ADX05977	Adx05977 Cyclin-de
_	8 2755.5	95.7	563	ω	ADS88282	Ads88282 Human pro
	9 2666.5	92.6	529	σ	ADX05979	Adx05979 Cyclin-de
Ä	0 2661	92.4	508	σ	ADX05981	Adx05981 Cyclin-de
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ñ	0 2384.5	82.8	569	7	AAY24054	Aay24054 A human b
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2	3 72384.5	82.8	269	٣	AAY96697	Aay96697 Human bet

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24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

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E3 ubiquitin ligase; beta-TrCP; F-box; WD protein; I-kappa-B; inhibitor; nuclear factor kappa-B; NF-kappa-B; degradation; modulator; anti-viral; anti-inflammatory; immunosuppressive; cytostatic.
                            AAY96696 standard; protein; 542 AA.
                                                                                                                                                  (first entry)
                                                                                                                                                                                                               Human E3 ubiquitin ligase.
                                                                                                                                               26-SEP-2000
                                                                                         AAY96696;
AAY96696
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WO200034447-A2 Homo sapiens. 15-JUN-2000 

99WO-US029371. 98US-00210060 09-DEC-1999; 10-DEC-1998; (SIGN-) SIGNAL PHARM INC. (YISS ) YISSUM RES & DEV CO.

Davis M; Ben-Neriah Y, Mercurio F, Amit S, Lavon I, Yaron A; Manning AM, Hatzubai A;

WPI; 2000-431294/37. N-PSDB; AAA51228 Polypeptide enhancing phosphorylated lkappaB ubiquitination useful for treating disorder associated with NF-kappaB activation e.g. cancer, comprising amino acid sequence of human E3 ubiquitin ligase or its variant.

Claim 1; Page 70-72; 77pp; English.

This is human E3 ubiquitin ligase (E3), which is homologous to human beta -TrCP, an F-box/WD protein family member. E3 enhances ubiquitination of phosphorylated I-kappa-B, an inhibitor protein of nuclear factor kappa-B (NF-kappa-B). Understanding I-kappa-B degradation via the ubiquitin pathway is useful for identifying modulators of this process for use in treating diseases associated with activation of NF-kappa-B. In vitro

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              functions as a dominant negative molecule in vivo. Transient over-expression of delta-beta-TrCP (a deletion mutant) inhibited the degradation of endogenous 1-kappa-B-alpha in stimulated Jurkat cells, resulting in accumulation of phosphorylated I-kappa-B-alpha. E3 can be used to screen for modulators of NF-kappa-B activity. E3 and beta-TrCP can be used to modulate NF-kappa-B to treat inflammatory diseases, autoimmune diseases, cancer and viral infections
suggests that deletion of the F-box results in a protein that
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Matches 542; Conservative
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity adactivity, i, immunomodulatory activity and activity, infinibin activity and may be useful in the diagnosis and/or treatment of cancer, leuksemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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Local Similarity 100.0%; Score 2879; DB 4;
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les 542; Conservative 0; Mismatches 0;
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Goodrich R;
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Wang D, Wang
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2000US-00588075.
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Xue AJ, Yang Y,
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, Zhao (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
                                                                                        SDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPA
                                                                                                                                                            GHRAAVNVVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQYRDRLVVSGS
                                                                     SDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPA
                                                                                                                                           STLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFLNVPPSAQNETRSPSRTYTYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peripheral nervous system, neuropathy; central nervous system; CNS; Alzheimer's, Parkinson's disease; Huntington's disease, haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemotactic; thrombolytic; drug screening; arthritis; inflammation;
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Zhang J
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Yang Y,
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Ε,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; SEQ ID NO 3353; 10078pp; English.
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rman T, Xu C, X
Drmanac RT;
                                                                                                                                                                                                                                                                                                                                              AAM40208 standard; protein; 542 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptide SEQ ID NO 3353.
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2000US-00488725.
2000US-00553117.
2000US-0058042.
2000US-00623450.
2000US-00653450.
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Wehrman T,
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21-JAN-2000;
25-APR-2000;
20-JUN-2000;
19-JUL-2000;
03-AUG-2000;
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19-OCT-2000;
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Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactis/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                 Sequence 542 AA;
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301 TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLV 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tumor; metastasis.
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                                                                                                                                                                                                                                                                                                                                                                               This invention relates to novel protein complexes of the tumour necrosis factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to methods for preparing these complexes comprises to the entended for preparing these complexes comprising at least two component proteins, as well as screening methods to identify modulators of the pathway, which include antibodies, agonists and antagonists thereof. The correct invention describes a protein complex and kit that are useful for diagnosing, prognosing or treating chronic inflammatory diseases such as septic shock and bacterial infections; neurological diseases such as served-induced inflammatory bowel disease; infectious diseases such as served-induced inflammatory neurodegenerative diseases and can served-induced inflammation in neurons; neurodegenerative diseases and can extra complexe complexes can be used for the development of pharmaceutical compositions that exhibit antihilammatory, antiarthritic, antirheumatic, cytostatic and antibacterial activities and can be used for gene therapy purposes. In particular, the invention further provides siRNA-oligonuclocides useful for inhibiting protein expression for in vitro or cell culture assays. This polypeptide is a human protein that can be used in combination with other proteins provided in the specification, to form novel complexes of the TNF-alpha signalling pathway
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                                                                                                                                                                                                                                                                             protein complex comprising at least one first and second protein of Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for
                                                                                                                                                                                                                                                                                           the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful fo
diagnosing or treating inflammation, neurological diseases, infectious
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100.0%; Pred. No. 2.8e-265;
ive 0; Mismatches 0;
                                                                                                                                                                                                    Ruffner H,
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                                                                                                                                                                                                     Bauch A,
                                                                                               24-SEP-2003; 2003WO-EP050655
                                                                                                                          26-SEP-2002; 2002EP-00021809
10-FEB-2003; 2003EP-00100274
                                                                                                                                                                                                     Huhse B, I
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Matches 542; Conservative
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                                                                                                                                                                         (CELL-) CELLZOME AG
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Superti-Furga G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 542 AA;
                                    WO2004035783-A2
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The present sequence is the protein sequence of human beta-transducin repeat containing protein 2 (beta-TrCP2). The invention provides a method of screening for an agent useful for sensitizing a cancer cell to DNA camage by a second agent. This involves: (i) contacting beta-TrCP with a test compound and a phosphorylated cell division cycle 25A (GGC25A) protein or its fragment; and (ii) detecting a reduced binding of the beta compound compared to a control. The second agent is e.g. ionizing cadiation or an alkylating agent. The beta-TrCP is beta-TrCP or peta-TrCP1 or beta-TrCP2. A second method involves: contacting a beta-TrCP with a test compound and a phosphorylated Cdc25A protein and detecting a reduced ubiquitin ligation of the phosphorylated Cdc25A protein in the presence of the test compound as compared to a control. A method of treating cancer involves administering a beta-TrCP inhibitor and a DNA damaging agent, where the beta-TrCP inhibitor sensitizes tumor cells in the patein to DNA damaging cancer troop by a damaging agent, where the beta-TrCP inhibitor is e.g. an antisense or
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                                                                                                                                                                                                                                       421 SDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPA
                                                                                                                                                                                                                                                                                                                                                             GHRAAVNVVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQYRDRLVVSGS
                                               361 GHRAAVNVVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQYRDRLVVSGS
                                                                                                                                                                              421 SDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPA
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short interfering RNA (siRNA) molecule. A method of reducing Cdc25A degradation in a cell involves reducing beta-TrCP activity by reducing the amount of beta-TrCP1 and/or TrCP2 in the cell e.g. by administering an antisense or siRNA molecule. The methods, inhibitors, agents, and compositions of the invention are useful for treating cancers, including metastatic and primary cancers, and cancers characterized by solid or non
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                                                                                                                                         Length 542;
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                                                                                                                                         Score 2879; DB 9;
Pred. No. 2.8e-265;
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Best Local Similarity
Matches 542; Conserv
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The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous adjectives, peripheral nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, anterities and inflammation, leuksemias and C.N.S disorders Note: The sequence data for this patent did not form
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                                                                                                                                                                                                                                                               Wang D;
, Zhao (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acids and polypeptides, useful for treating disorders as central nervous system injuries.
                                                                                                                                                                                                                                                               Ren F, Wa
Zhang J,
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Yang Y,
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Xue AJ,
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                                                                                                                                                                                                                                                               Asundi V, Chen R,
Wehrman T, Xu C,
R, Drmanac RT;
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                                                                                                                                                2000US-00623312.
2000US-00653450.
2000US-00662191.
2000US-00693036.
2000US-00727344.
                                                                                                          2000US-00488725.
2000US-00552317.
2000US-00598042.
                                                                   2000WO-US034263
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Best Local Similarity 100.
Matches 542; Conservative
                                                                                                                                                                                                                                                                              Wang Z, Weh
Goodrich R,
                                                                                                                                                                                                                                                                                                                       WPI; 2001-442253/47.
N-PSDB; AAI61150.
                                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                    HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 550 AA;
                                                                                                                                                  19-JUL-2000; 2
03-AUG-2000; 2
14-SEP-2000; 2
19-OCT-2000; 2
29-NOV-2000; 2
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25-APR-2000;
20-JUN-2000;
                                                                   26-DEC-2000;
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                           TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLV 368
                                                                                                                                           428
  TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLV
                                                                                                 GHRAAVNVVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQYRDRLVVSGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; cyclin-dependent kinase; cdk; biomarker.
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TNF-alpha; chronic inflammatory disease; rheumatoid arthritis;
inflammatory bowel disease; infectious disease; septic shock;
bacterial infection; neurological disease; stroke-induced inflammation;
neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
antirheumatic; cytostatic; antibacterial; gene therapy; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                   241 KGVYCLQYDDEKIISGLRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              361 GHRAAVNVVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQYRDRLVVSGS
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                                                                                                                                                                                                                                                                                                                                      61 RKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 STLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIMDFLNVPPSAQNETRSPSRTYTYI
                                                                                                                                                                    Gaps
directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This sequence represents a biomarker used in the method of the invention.
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                                                                                                                  Score 2873; DB 9;
Pred. No. 1e-264;
                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                       541; Conservative
                                                                                                                                              Similarity
                                                                          Sequence 542 AA;
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NGHKRGIACLOYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSG 459

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                                                                                                                                                                                                                                                                    This invention relates to novel protein complexes of the tumour necrosis factor-alpha (TNR-alpha) signalling pathway. Specifically, it refers to methods for preparing these complexes comprising at least two component proteins, as well as screening methods to identify modulators of the pathway, which include antibodies, agonists and antagonists thereof. The present invention describes a protein complex and kit that are useful for diagnosing, prognosing or treating chronic inflammatory diseases such as required should arthritis and inflammatory bowel disease; infectious diseases such as stroke-induced inflammation; neurological diseases such as stroke-induced inflammation in neurons; neurological diseases such as stroke-induced inflammation in neurons; neurological diseases such cancer. Accordingly, these complexes can be used for the development of pharmaceutical compositions that exhibit antilifilammatory, antiarthritic, can tirheumatic, cytostatic and antibacterial activities and can be used for gene therapy purposes. In particular, the invention further provides sixMA-oligonucleotides useful for inhibiting protein expression for in vitro or cell culture assays. This polypeptide is a human protein that can be used in combination with other proteins provided in the invention of the invention in the invention with other proteins provided in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESPKKSALWQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISRM 120
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                                                                                                                                                                  New protein complex comprising at least one first and second protein of
the Tumor Necrosis Factor-alpha(TNF-alpha)-signaling pathway, useful for
diagnosing or treating inflammation, neurological diseases, infectious
diseases or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGMLWKKLIERWYRIDPLWKGLSERRGWDQYLFKNRPIDGPPNSFYRSLYPKIIQDIETI
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Pred. No. 1.8e-253;
2; Mismatches 15; Indels
                                                                                                  Bauer A,
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                                                                                                  Ruffner H,
                                                                                                                                                                                                                                             Example; SEQ ID NO 137; 1980pp; English
                                                                                                   Bauch A,
24-SEP-2003; 2003WO-EP050655.
                            26-SEP-2002; 2002EP-00021809.
10-FEB-2003; 2003EP-00100274.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.7%;
Best Local Similarity 93.3%;
Matches 525; Conservative
                                                                                                  Bouwmeester T, Huhse B, I
Superti-Furga G, Kruse U;
                                                                     (CELL-) CELLZOME AG
                                                                                                                                           WPI; 2004-348460/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the invention
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whether a mammal will respond or is responding to an anti-cancer agent that modulates cyclin-dependent kinase (cdk) activity. The method comparises masuring the level of one or more blomarkers selected from comprises masuring the level of one or more blomarkers selected from 2774 biomarkers given in the specification (nucleotide sequence SEQ ID No:1246 (Genbank EST W28729) is especially preferred). The method of the invention is utilized in a kit for determining or predicting whether patient would be susceptible or resistant to treatment by an agent modulating cdk activity. The invention also describes a method for utilizing individualized genetic profiles for treating diseases and disorders based on patient's response and molecular level, specialized microarrays comprising the biomarkers described, antibodies directed gainst the biomarkers and a cell culture model to identify biomarkers. The cdk modulator is preferably N-5-[[5-(1,1-1])imethylethyl)-2- oxazolylmethyllthol-2-thiazolyl-4-piperidine carboxamide, 0.5-L-corporation acid salt. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp. wipo. intropublished pot sequences. This calculation carporation.
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421 NGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSG 480
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Pred. No. 5.2e-245;
1; Mismatches 4; Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cyclin-dependent kinase modulation biomarker SEQ ID NO 544.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cytostatic; cyclin-dependent kinase; cdk; biomarker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 544; 141pp; English.
                                                                                                                                                                                                                          542
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                                                                                                                                                                                                                                                            Biomarkers useful for predicting to a cancer treatment comprising
                                                                                                                                                                                                                             LNVPPSAQNETRSPSRTYTYISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADX05979 standard; protein; 529
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Best Local Similarity 92.4%;
Matches 512; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-2005 (first entry)
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dependent kinase activity
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dependent kinase activity

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DLQAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFLAVPPSAQN 528
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                                            QISNGTSSVIVSRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHIN 108
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                                                                                                                                                     ERMVRIDPLWKGLSESRGWDQYLFKNRPIDGPPNSFYRSLYPKIIQDIETIESNWRCGRH 215
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                                                                                                                                                                                                  216 NLORIQCRSENSKGVYCLQYDDEKIISGLRDNSIKIWDKTSLECLKVLTGHTGSVLCLQY 275
                                                                                                                                                                                                                                   DERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAVWDMA 348
                                                                                                                                                                                                                                                SATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIAC 408
                                                                                                                                                                                                                                                                                                                              LQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVW 468
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                                                                   95
                                                          36 QISNGTSSVIVSRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHIN
                                                                                                                                                                                                                                                                                                ----PRSLWLGCANLVESMCALSCLQSMPSVRCL
                                                                                          SYLKPMLQRDFITALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI
                                                                                                               96 SYLKPMIQRDFITALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLI
                                                                                                                                        ERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKIIQDIETIESNWRCGRH
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              Jackson DG,
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MEPDSVIEDKTIELM-CSV----
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N-PSDB; ADX05980.
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This invention describes a novel method of predicting or determining whether a mammal will respond or is responding to an anti-cancer agent that medulates cyclin-dependent kinase (cdk) activity. The method comprises measuring the level of one or more biomarkers selected from comprises measuring the level of one or more biomarkers selected from comprises measuring the level of one or more biomarkers selected from 2774 biomarkers given in the specification (nucleotide sequence SEQ ID NO:1246 (Genbank EST W28729) is especifically preferred). The method of the patient would be susceptible or resistant to treatment by an agent modulating cdk activity. The invention also describes a method for utilizing individualized genetic profiles for treating diseases and disorders based on patient's response and molecular level, specialized disorders based on patient's response and molecular level, specialized disorders based on patient's response and molecular level, specialized cagainst the biomarkers and a cell culture medel to identify biomarkers. The cdk modulator is preferably N-5-[[5-(1,1-1)-Dimethylethyl)-2-(2 against the biomarkers and a cell culture medel to identify biomarkers. The cdx modulator is preferably N-5-[[5-(1,1-1)-Dimethylethyl)-2-(2 cazolyl]methyl]thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-CC carrarric acid salt. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format compared to the printed specification, but was obtained for invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGVYCLQYDDEKIISGLRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 KGVYCLQYDDEKIISGLRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     447 STLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIMDFLNVPPSAQNETRSPSRTYTYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 RKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISRWCHYQHGHINSYLKPWLQRDFI
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Pred. No. 1.6e-244;
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Best Local Similarity 93.5%;
Matches 507; Conservative
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RESULT 11 AAM78583

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SDQVEFVEHLISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodilatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                       TIKVWNISTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHE
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nao QA, Wang D, Wang J, Zhang J, Ren F,
Yang Y, Wejhrman T, Goodrich R;
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01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-006549361.
20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
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27-APR-2000; 2000US-00560875.
20-JUN-2000; 2000US-00598075.
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N-PSDB; AAK51715.
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Ma Y, Zha
Xue AJ,
                  121
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                                                                                                                                                                                                                                                                                                                                                                                          임
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                leic acids encoding polypeptides with cytokine-like activities, useful diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CLNQETVCLASTAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSE 120
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                                                                                                            gene therapy;
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Wang
                                                                                                           Human, cytokine; cell proliferation; cell differentiation; gene the
vaccine; peptide therapy; stem cell growth factor; haematopolesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation.
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, Chen R,
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Wang D, Wang J, Zhang J, Ren F,
Wejhrman T, Goodrich R;
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2000US-00598075.
2000US-00620325.
2000US-00654936.
2000US-00693325.
2000US-00693325.
                                                                                  Human protein SEQ ID NO 1245.
                                                                                                                                                                                                                                                              05-FEB-2001; 2001WO-US004098
        AAM78583 standard; protein;
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Zhao QA, Wang L
, Yang Y, Wejhr
                                                          (first
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20-JUN-2000; 2
19-JUL-2000; 2
01-SEP-2000; 2
15-SEP-2000; 2
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                                                                                                                                                                                Homo sapiens
                                                          36-NOV-2001
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                                AAM78583;
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Ma Y, 2h
Xue AJ,
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ZW;

Y; Wang

Xu C, Cao , Chen R,

Human protein of a TNF-alpha signalling pathway protein complex Seq 129.

(first entry)

18-NOV-2004

ADS88274;

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunomodulatory activity and activity tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK5282) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 ITALPARGLDHIAENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKKLIERMVRTDSLWR 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDF 119
Nucleic acids encoding polypeptides with cytokine-like activities, useful
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                                                                                                                                                                                                                                                                                                                                            Length 605;
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                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                           1 MEP-DSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCL
                                                                                                                                                                                                                                                                                                                                           84.9%; Score 2445.5; DB 75.7%; Pred. No. 8e-224; ive 49; Mismatches 35
                                               20; Page 3503-3504; 6221pp; English
                    diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                              Matches 458; Conservative
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Best Local Similarity
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ADS88274 standard; protein; 605 AA.

RESULT 13 ADS88274 ID ADSE

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This invention relates to novel protein complexes of the tumour necrosis factor-alpha (TNF-alpha) signalling pathway. Specifically, it refers to methods for preparing these complexes comprising at least two component proteins, as well as screening methods to identify modulators of the pathway, which include antibodies, agonists and antagonists thereof. The correct invention describes a protein complex and kit that are useful for diagnosing, prognosing or treating chronic inflammatory diseases such as theumatoid arthritis and inflammatory bowel disease; infectious diseases such as stroke-induced inflammation in neurons; neurodegenerative diseases such as stroke-induced inflammation in neurons; neurodegenerative diseases and cancer. Accordingly, these complexes can be used for the development of pharmaccutical compositions that exhibit antiinflammatory, antiathritic, antirheumatic, cytostatic and antibacterial activities and can be used for the rapy purposes. In particular, the invention further provides is IRNA-oligonucleotides useful for inhibiting protein expression for in vitro or cell culture assays. This polypeptide is a human protein that can be used in combination with other proteins provided in the provision of the protein specification to form novel complexes of the TNF-alpha signalling pathway
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New protein complex comprising at least one first and second protein of the Tumor Necrosis Factor-alpha(TMP-alpha)-signaling pathway, useful for diagnosing or treating inflammation, neurological diseases, infectious diseases or cancer.
                                                                                                                               protein complex; tumour necrosis factor-alpha signalling pathway;
INF-alpha; chronic inflammatory disease; rheumatoid arthritis;
inflammatory bowel disease; infectious disease; septic shock;
bacterial infection; neurological disease; stroke-induced inflammation;
neurodegenerative disease; cancer; antiinflammatory; antiarthritic;
antirheumatic; cytostatic; antibacterial; gene therapy; human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bauch A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                26-SEP-2002; 2002EP-00021809.
10-FEB-2003; 2003EP-00100274.
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Best Local Similarity 75.73
Matches 458; Conservative
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83 MPSLRCLYNPGTGALTAFONSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNOETV 142
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MDPABAVLQEKALKFMMEFRSWCPGWNTWARSRLTATSTSRVQCSMPRSLWLGCSSLADS
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84.2%; Score 2423; DB 4;
Best Local Similarity 72.5%; Pred. No. 1.3e-221;
Matches 458; Conservative 49; Mismatches 35;
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               WPI; 2001-476283/51.
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Vang D, Wang J, Zhang J, Ren F, Chen R, Wang
                                                                                                                                                                                                                                                                                                                                                                                                                         Human, cytokine; cell proliferation; cell differentiation; gene the vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
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19-JUL-2000; 2000US-00620325.
01-SEP-2000; 2000US-00654936.
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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to prytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymeries in other cell populations or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopoiesis regulating activity tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
                                                                                                                                                                                                                                                 Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
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     Goodrich
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     Wejhrman T,
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Wang D, Wang J
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20-JUN-2000; 2000US-00598075.
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Xue AJ, Yang Y,
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283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0°, Gapext 0.5 Searched: 283416 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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RESULT 1 B48088 beta-transducin repeat-containing protein - African clawed frog N;Alternate names: beta-Trcp C;Species: Xenopus laevis (African clawed frog) C;Dete: 26-May-1994 #sequence_revision 26-May-1994 #text_change 05-Oct-2004 C;Accession: B48088	R;Spevak, W.; Keiper, B.D.; Stratowa, C.; Castanon, M.J. Mol. Cell. Biol. 13, 4953-4966, 1993 A;Title: Saccharomyces cerevisiae cdc15 mutants arrested at a late stage in anay A;Reference number: A48088; MUID:93330289; PMID:8393141	A;Accessaton: B48U88 A;Status: preliminary A;Molecule type: mRNA A;Residuse: 1-518 <spr- 1-518="" <spr-="" <wdi="" a;cross-references:="" a;residuse:="" domain:="" duplication="" f;431-462="" gb:m98268;="" homology="" nid:g2955:c;reywords:="" repeat="" uniparc:upi0000137338;="" uniprot:q91854;="" wd=""></spr->	Query Best Match	දුරු සු
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n anaphase arr

g295542; PIDN

HGHINSYLKPMLQRDFITALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGML 163

104 94 164

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WKKLIERMVKTDPLWKGLSERRGWDQYLFKNRPTDG--PPNSFYRSLYPKIIQDIETIES

NWRCGRHNLORIOCRSENSKGVYCLOYDDEKIISGLRDNSIKIWDKTSLECLKVLTGHTG

222

IAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLNG 401 

274 342

282

SVLCLQYDERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRS

HKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAY 461

402 394 462

DGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFLN 521

221

281

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A;Accession: T50211
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: UNPROT:Q09855; UNIPARC:UPI0000131DC4; EMBL:AL136538; PIDN:CAB66464..
A;Cross-references: Strain 972h(-); cosmid c30
C;Genetics: spAc2956.01; SPDB:SPAC30.05
A;Map position: 1
A;Introns: 43/1; 74/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: UNIPROT:P87053; UNIPARC:UPI0000131DBA; EMBL:294864; PIDN:CAB08168.1; A,Experimental source: strain 972h-; cosmid c57A10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     probable sulfur metabolite control protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                              14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----HNLQRIQCRSENS-----KGVYCLQYDDEKIISGLRDNSIKIWDKTSLECLKVLT 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----FNTGEQHCVLHNSRNSRVFGLÖFDHRR 482
                                                                                                                                                                                                                                                                                                                                      93
                                                                                                                                                                                                                                                                                                                                                                                                 | :|: | :|: : : :| | CKCKLMSKRWKRLLEDPGIWKALY -----MQKGWFVNENVLNEFEAWRRTHKFPQPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FENFLKQQNIIGPYGTMFLPQQFIF----SSNGRPLLNWSYLY----KEHAHLDSNWRHGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 278 GHTGSVLCLQYDER---VIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 336 CSKDRSIAVW--DMASATDITLRRVLVGHRAAVNVVDFDDK--YIVSASGDRTIKVWSTS
                                                                                                                                                                                                                                                                                               ESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALPEQGLDHIAENILSYLDARSL
                                                                                                                                                                                                                                                                                                                            ----DQYLFKNRPTDGPPNSFYRSLYPKIIQDIETIESNWRCGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF
                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: T38932
K;Badcock, K; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, April 1997
A;Reference number: Z21818
                                                                                                                                                                                                                                                              95;
                                                                                                                                                                                                                                                                                                                                                                           145 CAAELVCKEWQRVISEGMLWKKLIERMVRTDPLWKG-----LSERRGW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 605;
                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                         23.7%; Score 683.5; DB 2;
31.3%; Pred. No. 6.1e-44;
ive 98; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.3%; Score 584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438 NDEKIVSGGYDGTVRIWN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IISSSHDDTILIWDF 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IIACTHSSEILVWNF 497
                                                                                                                                                                                                                           Query Match 23.76
Best Local Similarity 31.35
Matches 155; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SPDB:SPAC57A10.05c
 Reference number: Z25046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-605 <BAD>
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A, Gene: SPL
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Up-repeat protein [imported] - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 05-Oct-2004
C;Accesabior: TS0211
R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Murphy, L.; Jones, L.; Mc, Submitted to the EMBL Data Library, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: UNIPARC:UP1000017BAB4; EMBL:U28730; NID:g860694; PID:g860695; PIDN:A
A,Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ω,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALPEQGLDHIAENILSYLDA 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :||| :|:: :: |: || | :::::|||||||| :::
KWSEHEQLDFMDKIVHRLSHYQLGKVDNFIRPMLQRDFISNLPA----HLVELILFNVNS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 SKGVYCLQYDDDKIVSGLRDNTIKIMDRKDYSCSRILSGGHTGSVLCLQYDDRVIISGSSD 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGHRAAVNVVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQYRDRLVVSG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGHRAAVNVVDFDDRYIVSASGDRTIKVWSMDTLEFVRTLAGHRRGIACLQYRGRLVVSG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  142 RSLCAAELVCKEWQRVISEGMLWKKLIERMVRTDPLWKGLSERRGWDQYLFKNRPTDGP- 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRRVL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAP 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  513
                                                                                                                                                                               Apporthetical protein K10B2.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16607
R;Miller, N.
Submitted to the EMBL Data Library, June 1995
A;Description: The sequence of C. elegans cosmid K10B2.
A;Reference number: Z18545
A;Accession: T16607
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-701 <MIL>
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-- PNSFYRSLYPKIIQDIETIESNWRCGRHNLORIOCRSEN
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A;Introns: 78/3; 125/1; 183/2; 281/3; 404/3; 551/3; 668/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1638.5; DB 2 Pred. No. 4.3e-116;
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Best Local S
Matches 309
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A,Cross-references: UNIPROT:Q01277; UNIPARC:UPI000013566D; EMBL:U17251; NID:g806757; PID
C,Genetics:
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C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 05-Oct-2004
C;Accession: T46660
R;Kumar, A.; Paietta, J.V.
Rp.c. Natl. Acad. Sci. U.S.A. 92, 3343-3347, 1995
A;Title: The sulfur controller-2 negative regulatory gene of Neurospora crassa encodes
A;Reference number: Z23121; MUID:95241499; PMID:7724564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYS3
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                     --YOKEKDL--CIKYFDQWSESDQVEFVEHLISRMCHYQHGHINSYLK 112
                                                                                                                 PMLQRDFITALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLIERMV 172
                                                                                                                                                                  177 HMIKIDFISILPQE----LSLKILSYLDCQSLCNATRVCRKWQKLADDDRVWYHMCEQHI 232
                                                                                                                                                                                                                                                                      ------DRKCPNCGWGLPLLHMKRARIQQNSTGSSSNADIQTTRPWKVIYRERF 282
                                                                                                                                                                                                                                                                                                                                                     DKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLH 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                    | : : : |:||: | : |:|| | 328 DLFTGKLIRRLSGHSDGVKTLYFDDRKLITGSLDKTIRVWNYITGECISTYRGHSDSVLS 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           326 LRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYI--VSASGDR 383
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                                                 PKIIQDIETIESNWRCGRHNLQRIQCRSENSK----GVYCLQYDDEKIISGLRDNSIKIW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --- PTDGPPNSFYRSLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 650;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Accession: T46660
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-650 <KUM>
                                                                                                                                                                                                                       RTDPLWKGLSERR----GWDQYLFKNR---
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RIISGSHDGSIKVWDLQ-
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Matches 155, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           515 LIWDFLNVPPSA 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Introns: 75/3; 319/1; 354/1
C; Function:
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                       KRPSEGN-
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                                                                                                                        113
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                       62
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84932
MET30 protein - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein Y19905.02; protein Y1L046w
C;Species: Saccharomyces cerevisiae
C;Date: 28-May-1993 Hequence_revision 24-Feb-1995 #text_change 05-Oct-2004
C;Accession: 849932; 843750
R;Odell, C; Bowman, S.
submitted to the EMBL Data Library, December 1994
A;Reference number: 849931
A;Accession: 849932
A;Accession: 849931
A;Accession: 849932
A;Accession: 849930
A;Accession: 84950
A;Accession: 84750
A;Cross-references: UNIPROT: P39014; UNIPARC:UPI000012F726; GB:Z47047; EMBL:Z46861; NID:G submitted to the EMBL Data Library, December 1993
A;Reference number: 843750
A;Accession: 843750
A;Ac
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                                                                                                                                                                                                                                                                                                                                                                                                          267 VVLSGHSDGVMCLQLVRNILASGSYDATIRLWNLATFQQVALLEGHSSGVTCLQFDQCKL 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::|| | |:|:|: | | :: | | ::|| | :|| | :|| | 327 ISGSMDKTIRIWNYRTSECISILHGHTDSVLCLTFDSTLLVSGSADCTVKLWHFSGGKRI 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLRRVLVGHRAAVNVVDF--DDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQY 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              154 CEQHINRKCEKCGWGLPLLERNTLYAAKASIQKRYERLTKRGVDQAHESSPVKKAKLDDY 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   412 RDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQ 471
                                                                                                         STIDSLVRLDFLSLLPVE----ISFRILSFLDARSLCQAAQVSKHWKELADDDVIWHRM
                                                                                                                                                                                                                                                                                                         TLR----GHTGPVNSVRIIRDRGLVLSGSDDSTIKIWSLETNTCLHTFSAHIGPVQSLAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFLNVPPSAQNETR
                                                                      NSYLKPMLQRDFITALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKL
                                                                                                                                                                          IER-----RRGWDQY-----LFKNRPTDG
                                                                                                                                                                                                                                                                            ----PNSFYRSLYP-----KIIQDIETIESNWRCGRHNLQRIQCR-
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                       82;
                       Indels
Pred. No. 2.7e-36;
85; Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Map position: 9L
F;298-329/Domain: WD repeat homology <WD1>
F;338-369/Domain: WD repeat homology <WD2>
F;374-409/Domain: WD repeat homology <WD3>
F;417-450/Domain: WD repeat homology <WD4>
30.6%;
                          147; Conservative
  Similarity
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& a & a	383 RTIKVWSTSTCEFVRTLNGHKRGIACLOYRDRLVVS 418	A,Residue A,Cross-r A,Experim C,Genetic A,Gene: C. A,Map pos	A; Residues: 1-579 <wil> A; Coss-references: UNIPROT: Q93794; UNIPARC: UPI0000135742; EMBL: Z79757; PIDN: CAB02129.1; A; Cross-references: UNIPROT: Q93794; UNIPARC: UPI0000135742; EMBL: Z79757; PIDN: CAB02129.1; A; Genetics: CESP: F55B12.3 A; Gene: CESP: F55B12.3 A; Map position: 5 A; Introns: 22/3; 45/2; 77/3; 122/3; 171/2; 211/2; 342/2; 417/3; 478/3; 526/1</wil>
ζ Q	420 SSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDERAP 479 	Query M Best Lo Matches	<pre>Query Match 17.8%; Score 512; DB 2; Length 579; Best Local Similarity 27.5%; Pred. No. 7.2e-31; Matches 146; Conservative 77; Mismatches 206; Indels 102; Gaps 15;</pre>
% da	480 ASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDF 519 606 RSGKCDATYTGHCGPVTCVGLSDSLMASGSEDGTIRLHSF 645	ζζ Dp	51 SNGTSSVIVSRKRPSEGNYQKEKDLCIKYPDQWSESDQVEFVEH 94    :   :
RESULT 7 S62507 S62507 S62507 C; Species: Si C; Accession: R; Jones, L.; Submitted to A; Ractence to A; Ractence to A; Ractence to A; Racsidues: pr A; Residues: pr A; Residue	HEBULT 7  S62507  Hypothetical trp-asp repeat-containing protein - fission yeast (Schizosaccharomyces pombly contential trp-asp repeat-containing protein - fission yeast (Schizosaccharomyces pombly Spaces Schizosaccharomyces pombly Cipate: 12-Feb-1998 #text_change 05-Oct-2004  Cipate: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 05-Oct-2004  Cipate: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 05-Oct-2004  Ridones Li Murphy, Li, McNeil, A.; Simpson, II; Harris, D.; Barrell, B.G.; Rajandream, Mcleater number: 221798  A; Reference number: 221798  A; Reference number: 221798  A; Scatus preliminary  A; Residues: 1-267 <-AO2> A; Status preliminary  A; Cross references: UNIPARC:UPI0000169029; EMBL:266525; NID:g1044926; PIDN:CAA91423.1; F C; Genetics:  C; Genetics: A; Map position: 1  F; 18-51/Domain: WD repeat homology <-WDI> F; 19-51/Domain: WD repeat homology <-WDI> Ouery Match  Query Match  A; Mismatches B5; Indels 29; Gaps 6;  Matches 106; Conservative 54; Mismatches B5; Indels 29; Gaps 6;  A; Mismatches 106; Conservative 54; Mismatches B5; Indels 29; Gaps 6;  A; H	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	95 LISRMCHYQHGHINSYLKPMLQRDFITALPEQGLDHIABNILLSYLDARSLCAAELVCKEW 154  1 LLQESNITHIRQLAALIEPHFQREDENCELVEGAMKILHNITGYDLLKVAQVSKAW 146  155 QRVISEGMLWKKLIERMYRTDPLWKGLSERKGMOQYLFKNRPTDGPPDSF

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Accession: T40157
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WD-40 repeat protein [imported] - Nostoc sp. (strain PCC 7120)

C;Species: Nostoc sp. PCC 7120

A,Note: Nostoc sp. strain PCC 7120

B,Rocession: AE1810

R,Raneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

R,Raneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

R,Razaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

DNA Res. S. 205-213, 2001

A;Reference number: AB1807; MUID:21595285; PMID:11759840

A;Reference number: AB1807

A;Reterence number: Asim Ana

A;Reterence number: Asim A;Reterence number:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKPMLQRDFITALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLIER 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MVRIDPLWKGLSERRG--WDQYLFKURPIDGPPNSFYRSLYPKIIQDIETIESNWRCGRH 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHEELVRCIRFDNKR - - IVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRL
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LLPIFQKNFLTGFPAE----ITNLVLTHLDAPSLCAVSQVSHHWYKLVSS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15.7%;
26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 135; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                    A;Residues: 1-775 <KOM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21
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RESULT 9
T18511
beta transducin-like protein - Podospora anserina
C;Species: Podospora anserina
C;Species: Podospora anserina
C;Species: Podospora anserina
C;Species: Doct-1999 #sequence_revision 15-oct-1999 #text_change 09-Jul-2004
C;Accession: T18521
R;Saupe, S.; Turcq, B.; Bequeret, J.
R;Saupe, S.; Turcq, B.; Bequeret, J.
R;Saupe, S.; Turcq, B.; Bequeret, J.
A;Title. A gene responsible for vegetative incompatibility in the fungus Podospora anser
A;Reference number: 218944; MUID:96009891; PMID:7557402
A;Reference number: 218944; MUID:96009891; PMID:7557402
A;Roccusion: T18521
A;Roccusion: T18521
A;Roccusion: T1852
A;Roccusion: Distribution anser
A;Residues: 1-1356 «SAU»
A;Roccusion: 1-1356 «SAU»
A;Roccusion: 1-1356 «SAU»
A;Roccusion: 1-1358 (SAU)
A;Roccusion: 
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T45136

T45136

Cynecies: Schizosaccharomyces pombe
Cynecies: Schizosaccharomyces pombe
Cynecies: Schizosaccharomyces pombe
Cynecies: Schizosaccharomyces pombe
Cynecies: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
Cynecesion: T45136; T40157
Rykominami, K.; Toda, T.
Rykominami, T.
Rykominami, T.
Rykominami, Toda, T.
Rykominami, T.
Rykominami, T.
Rykominami
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DHI--AENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLIERMVRTDPLWKGLSERRG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHEELVRCIRF--DNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRL 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLECLKVLTGHTGSVLCLQY - - DERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIYWIDHLR-----DLVSSTSSKWVHLLQDDGDIHRFLTTKYLYWLEALSLLRALPE-GI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAİRQLESLİGHTIRGRİJA-----IVRDGYRFALSYRMIJEKAPLQAYTS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --ALVF--APTDSMIKKIFKKEEPGWISTISVVEAEWNACTQTLEGHGSSVLSVAFSADG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QRIQCRSENSK------GVYCLQY--DDEKIISGLRDNSIKIWDKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFS-NGLMVTC-SKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDF--DDKYIVSASGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 16.3%; Score 468.5; DB 2; Best Local Similarity 28.7%; Pred. No. 4.6e-27; Matches 144; Conservative 74; Mismatches 189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFSPDGQRVASGSIDGTIKIWD 1163
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A;Cross-references: UNIPARC:UPI0000143E17; EMBL:X05625; NID:g3502; PIDN:CAA29113.1; PID::R;Murakami, Y.
                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPARC:UP10000127254; EMBL:D31600; NID:9836814; PIDN:BAA06495.1; PII
R;Yochem, J.; Byers, B.
J. Mol. Biol. 195, 233-245, 1987
A;Title: Structural comparison of the yeast cell division cycle gene CDC4 and a related A;Reference number: A26867; MUID:88011240; PMID:3309335
A;Accession: A26867
A;Molecule type: DNA
A;Residues: 1-459, E',461-779 < YOC>
                                                                                                                                                                                                                                                                                                                                                                                                                                          the spindle pole bodies to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                306 NKIIRKSTSLWKKLL-----LSENFVSPKGFNSLNLK-----LSQKY 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PKIIQD-----IET--IESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISGLRDN 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 320 NEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDD----KY 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 SIKIWDKTSLECLKVLTGHTGSVLCLQYDE-RVIVTGSSDSTVRVWDVNTGEVLNTLIHH 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----STCE----FVRTLNGHKRGIACLQYR 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480 IVTGSRDNTLHVWKLPKESSVPDHGEEHDYPLVFHTPEENPYFVGVLRGHMASVRTVSGH 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            413 DRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDN--KRIVSGAYDGKIKVWDL 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F-box/WD-repeat protein pop2 - fission yeast (Schizosaccharomyces pombe)
N;Alternate names: proteolysis factor sudlp
C;Species: Schizosaccharomyces pombe
C;Date: 21-Jan-2000 #sequence revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43557; T38794; T43798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q-----AALDPRAPASTL--CLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------HVFKGHNSTVRCLDIVEYKNIKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LISRMCHYQHGHINSYLKPMLQRDFITALPEQGLDHIAENILSYLDARSLCAAELVCKEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QRVISEG-MLWKKLIERMVRTDPLWKGLSER----RGWDQYLFKNRPTDGPPNSFYRSLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 132;
                                                                                                                                                                                                                                                                                                                                                                                                                 C.Function:
A,Description: initiation of DNA replication; separation of C;Reywords: cell cycle control
F,459-494/Domain: WD repeat homology <WD1>
F,628-659/Domain: WD repeat homology <WD2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 14.5%; Score 418; DB 2; Best Local Similarity 25.5%; Pred. No. 1.4e-23; Matches 128; Conservative 82; Mismatches 160
                                                                                                                                                                                        A,Reference number: $62302
A,Reference number: $62302
A,Accession: $63204
A,Accession: $63204
A,Recalle type: DNA
A,Residues: 1-779 <MUM>
                                                                                                                                                                                                                                                                                                                                                                         SGD:S0001885; MIPS:YFL009w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----ANDYSRKFSYHHTNLS 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 IVSASGDRTIKVWST-----
                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 6L
                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Gene: SGD:CDC4
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N.Alternate names: protein YFL009w
N.Alternate names: protein YFL009w
N.Alternate names: protein YFL009w
N.Alternate names: protein YFL009w
C.Species Saccharomyces cerevision 12-Apr-1996 #text_change 05-Oct-2004
C.Accession: S56445; 848310; AZ6667; S62304
C.Accession: S56445; 848310; AZ6667; S62304
A.Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces of A.Accession: S5648
A.Molecule type: DNA
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-779 <MUR>
A.Gross-references: UNIPROT: P07834; UNIPARC: UPI0000127254; EMBL: D50617; NID: 9836685; PIC
R.Churcher, C.
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                    A;Cross-references: UNIPROT:QBZOR1; UNIPARC:UP100000CDBE5; GB:BA000019; PIDN:BAB77553.1; A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr0029
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A;Reference number: S48310
A;Accession: S48310
A;Molecule type: DNA
A;Residues: 1-579 < CHU>
A;COS8-references: UNIPARC:UPI0000168A6E; EMBL:Z46255; NID:g559925; PIDN:CAA86341.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSPDSRMLASGSADSTIKLWDVHTGECLKTLSKNTNKVYSVAFSPDGRILASASQDQTIK 711
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                                                                                                                                                                                                                                                                                                               IKYFDQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFITALPEQGLDHIAENIL 136
                                                                                                                                                                                                                                                                                                                                                                                                    SYLDARSLCAAELVCKEWQRVISEGMLWKKL.----IERMVRTDPLWKGLSERRG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W-----DQYLFKNRPTDGPPNSFYRSL-----YPKIIQDIETIESNWRCGRHN 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQRIQCRSENSKGVYCLQY--DDEKIISGLRDNSIKIWDKTSLECLKVLTGHTGSVLCLQ 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y--DERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFS--NGLMVTCSKDRSIA 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VWDWASATDITLRRVLVGHRAAVNVVDF----DDK--YIVSASGDRTIKVWSTSTCEFVR 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLNGHKRGIACLQYR - - DRLVVSGSSDNTIRLWDIECGACLRVLECHEELVRCIRF - - DN 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQF--DEFQIISSSHD 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTLASCGEDRSIKLWDIQRG-----ECVNTLWGHSSQVWAIAFSPDGRTLISCSDD 879
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                                                                                                                                                                                                                         WIGCANLVESMCALSCLQSMPSVRCLQISNGTSSVIVSRKRPSEGNYQKE-----KDLC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.8%; Score 425; DB 2; Length 1227;
llarity 25.3%; Pred. No. 7.9e-24;
Conservative 106; Mismatches 192; Indels 112;
                                                                                                                                                                                                                                                                                                                                                       455 MEYI-----TAKFIENSLEEF-----SQTKKL---DFINTYP
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           A;Residues: 1-1227 <KUR>
                                                                                                                                      Query Match
Best Local Similarity
Matches 139; Conserv
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A12493
WD-repeat protein [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120alpha
C5, Species in Nostoc sp. PCC 7120
A; Nostoc sp. strain PCC 7120
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C; Date: 14-Dec-201 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C; Date: 14-Dec-201 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C; Date: 14-Dec-201 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C; Date: 10-Nakamara, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Res. 8, 205-213, 2001
A; Reference number: AB1807; MUID:21595285; PMID:11759840
A; Accession: A12493
A; Accession: A12493
A; Accession: A12493
A; Residues: 1-1189 < KUR>
A; Residues: 1-1189 < KUR>
A; Residues: 1-1189 < KUR>
A; Cross-references: UNIPROT:Q8YL09; UNIPARC:UPI00000CEEDC; GB:BA000020; PIDN:BAB78213.1, A; Experimental source: strain PCC 7120
C; Genetics:
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AC1842

AC1842

AC1842

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AC1842

AC262168: Nostoc sp. PCC 7120

A,Note: Nostoc sp. PCC 7120

A,Note: Nostoc sp. strain PCC 7120

A,Note: Nostoc sp. strain PCC 7120

A,Note: Nostoc sp. strain PCC 7120

A,Note: Nostoc sp. strain PCC 7120

A,Note: Nostoc sp. strain PCC 7120

A,Rocession: AC1842

C,Accession: AC1842

C,Accession: AC1842

A,Rameko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi

B,Akzaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S

BNA Res. 8, 205-213, 201

A,Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A,Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 DEKIISGLRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDER--VIVTGSSDSTVRVWDV 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     308 NTGEVLNTLIHHNEAVLHL--RFSNGLMVTCSKDRSIAVWDM-----ASATDITLRRVL 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQII 506
                                                                                                         VVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF -- DNKRIVSGAYDGKIKVWDLQ-- 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               360 VGHRAAVNVVDFDD--KYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQYR--DRL
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                                                                                                                                                                                                                               SSSHDDTILIWDFLN 521
                                                                                                                                                                                                                                                                                                          AAVQRDDQAYLEVIN 697
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Best Local Similarity
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                                                             447
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Riwolf, D.A.; Jackson, P.K.

Submitted to the BMBL Data Library, December 1997

A; Description: Fission yeast pop2 encodes a novel F-box/WD-repeat protein involved in the A; Description: Fission yeast pop2 encodes a novel F-box/WD-repeat protein involved in the A; December 222576

A; Reference number: 222576

A; Reterance number: 222576

A; Redatus: 1-703 - 4WDL.

A; Residues: 1-703 - 4WDL.

A; Residues: 1-703 - 4WDL.

A; Residues: UNIPARC: UNIPARC: UPI0000131F36; EMBL: AF038867; FIDN: AAB95480.

A; Residues: CA: Bara Library, August 1996

A; Residues: CA: Churcher C M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

B; Rigartles, S; Churcher: CA: Barrell, B.G.; Rajandream, M.A.; Wood, V.

B; Rigartles, S; Churcher: CA: Sarrell, B.G.; Rajandream, M.A.; Wood, V.

B; Rigartles, S; Churcher: CA: Sarrell, B.G.; Rajandream, M.A.; Wood, V.

B; Rigartles, Drailminary; translated from GB/EMBL/DDBJ

A; Residues: 1-703 - GEN,

A; Reference number: 222686; MUID: 98138628; PMID: 9653157

A; Reference number: 222686; MUID: 98138628; PMID: 9653157

A; Reference number: 222686; MUID: 98138628; PMID: 9653157

A; Reference number: 222686; MUID: 98138628; PMID: 9653157

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A; Reference number: 222686; MUID: 98138628; PMID: 9653157

A; Reference number: 222686; MUID: 981382; PMID: 98293382; PIDN: A; Reference number: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: PWID: P
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Gaps

51;

Length 1189; Indels

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A;Accession: AC1842
A;Status: preliminary
A;Batatus: preliminary
A;Batatus: L-1747
A;Residus: L-1747
A;Gene: allo283
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                                                                                                                                                                                                                                                                                                                        1468 SLSTIQ---KNQNIITTVSYSPDGKTIATASADNTIKLMDSQTQQLIKTLTGHKDRITTL 1524
                                                                                                                                                                                                                               229 NLQRIQCRSENSKGVYCLQY--DDEKIISGLRDNSIKIWDKTSLECLKVLTGHTGSVLCL 286
                                                                                                                                                                                                                                                                                                    287 QY--DERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFS--NGLMVTCSKDRSI 342
                                                                                                                                                                                                                                                                                                                                                                        343 AVWDMASATDITLRRVLVGHRAAVNVVDF--DDKYIVSASGDRTIKVWSTSTCEFVRTLN 400
                                                                                                                                                                                              19; Gaps
                                                                                                                                                         Query Match
Best Local Similarity 33.5%; Pred. No. 1.8e-20;
Matches 85; Conservative 51; Mismatches 99; Indels 19;
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1701 LSGGEDAGVMVWNL 1714
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Search completed: August 25, 2006, 07:23:15 Job time : 44 secs

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GenCore version 5.1.9
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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- protein search, using sw model OM protein

August 25, 2006, 07:14:17; Search time 303 Seconds (without alignments) 1654.648 Million cell updates/sec Run on:

US-10-665-715-16 Perfect score: Title:

542 1 MEPDSVIEDKTIELMCSVPR......PPSAQNETRSPSRTYTYISR Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2849598 segs, 925015592 residues Searched:

2849598 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: uniprot\_sprot:\*
2: uniprot\_trembl:\* UniProt 7.2:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	homo	7 mus	mus	gnw	E	mus	Q3tgm9 m 17 days e		Q5zhq9 gallus gall		homo	homo	แนย		Q68ds0 homo sapien			5 macac	2 homo	mus m	mus	mus	Q9r1g7 mus musculu	rattus n	4 xenopus	Q6ax69 xenopus lae		~		m	Q7pyh7 anopheles g
ID	FBW1B_HUMAN	Q5SRY7_MOUSE	Q8K022_MOUSE	Q923H0 MOUSE	Q8BY90_MOUSE	Q3TLZ8 MOUSE	Q3TGM9_MOUSE	Q8CHD5_MOUSE	Q52HQ9 CHICK	Q6PGW4_BRARE	FBW1A HUMAN	QSW141 HUMAN	Q3ULA2_MOUSE	Q571K6_MOUSE	Q68DS0_HUMAN	Q5RDW6_PONPY	Q7ZVZ1_BRARE	Q4R6Z6 MACFA	Q5W142_HUMAN	Q9QUI5_MOUSE	Q9Z159 MOUSE	Q3U0Q4_MOUSE	Q9R1G7 MOUSE	QSU4ES RAT	TRCB XENLA	Q6AX69_XENLA	Q4T8J7 TETNG	Q86SD3_CIOIN	044382_DROME	Q9VDE3_DROME	Q7PYH7_ANOGA
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% Query Match	100.0	99.8		95.7	95.6	92.5	92.4	92.4	92.1		84.9	84.9			•		•	83.5	82.8		٠	ς.	•	٠.	79.9	79.9	4.		72.2		70.8
Score	2879	2872	2851.5	2755.5	2665.5	2664.5	2660	2660	2652.5	2448.5	2445.5	2445.5	2437.5	2436.5	2434	2429.5	2423.5	2403	2384.5	2375.5	2368.5	2362	2356.5	2353.5	2301	2301	2157	2114.5		077.	2039.5
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## ALIGNMENTS

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Mammalia, Butheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Butchow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20003060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;
Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M.,
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MEDLINE=98403880; PubMed=9734811; DOI=10.1093/dnares/5.3.169;
Ishikawa K., Nagase T., Suyama M., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Prediction of the coding sequences of unidentified human genes. X. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";

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MEDILINE=20160458; PubMed=10694485; DOI=10.1006/bbrc.2000.2241;
Kolke J., Sagara N., Kirikoshi H., Takagi A., Miwa T., Hirai M.,
Katoh M.;
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [MRNA], AND ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM B).
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542 AA.
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PRT;
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NUCLEOTIDE SEQUENCE [MRNA]
STANDARD;
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FBW1B HUMAN
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Hopkins B.;
Submitted (FEB-2005)
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Rahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Raheseley R.W., Touchman J.W., Green E.D., Dickson M.C., Sanchez A.C., Grimwood J., Schmutz J., Myers R.M., Blakealey R.W., Krzywinski M.I., Skalska U., Smailus D.E., Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., A. Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; "Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

- FUNCTION: Probably recognizes and binds to some phosphorylated proteins and promotes their ubiquitination and degradation. May participate in Wnr signaling.

- I- FUNCTION: Probably recognizes and binds to some phosphorylated participate in Wnr signaling.

- I- SUBCELLULAR LOCATION: Cytoplasm (Potential).

- ALTERNATIVE PRODUCTS: Named incfermed and complex.

- LALTERNATIVE PRODUCTS: Named incfermed and complex.

- LALTERNATIVE PRODUCTS: Named incfermed and complex.
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WD 2.
WD 3.
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WD 5.
WD 6.
WD 6.
WD 6.
YD 7.
WD 6.
CSVPRSIMEGCANLVESMCALSCLQSMPSVRCL -> NTSV
                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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R HGNC; HGNC:13607; FBXW11.

R HGNC; HGNC:13607; FBXW11.

R GD: GO: 00010515; C: ubiquitin ligase complex; NAS.

R GO: 00010515; E: protein binding; IPI.

GO; GO: 00016567; P: protein binding; IPI.

GO; GO: 0016567; P: protein ubiquitination; NAS.

R InterPro; IPR001810; F-box.

R InterPro; IPR001810; F-box.

R Ffam; PF00460; WD40.

R PFam; PF00400; WD40.

R R PANYS; RR00320; GPROTEINBRPT.

R RNART; SM00320; GPROTEINBRPT.

R RNART; SM00320; WD40; 1.

R RNART; SM00320; WD40; 7.

R RNART; SM00320; WD40; 7.

R RNASTE; PS50181; FBOX; 1.

R RNOSITE; PS50023; WD REPEATS_2; 7.

R RNOSITE; PS50024; WD REPEATS_2; 7.

R RNOSITE; PS50029; WD REPEATS_2; 7.

R Alternative splicing; Repeat; Ubl conjugation pathway; WD repe
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/FTId=PRO_000050981.
F-box.
                                                                                                                                                                                                                              Event-Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                EMBL, AF176022; AAF04528.1; -; mRNA.
EMBL, AB03329; BAA92329.1; -; mRNA.
EMBL, AB033280; BAA92330.1; -; mRNA.
EMBL, AB033281; BAA92331.1; -; mRNA.
EMBL, AB04595; BAA31671.1; ALT INNT; mRNA.
EMBL, BC056213; AAH26213.1; -; mRNA.
HSSP, Q9Y297; 1P22.
                                                                                                                                                                                                                                                                                                          lsoId=Q9UKB1-3; Sequence=VSP_006766;
dILARITY: Contains 1 F-box domain.
                                                                                                                                                                                                                                                                                  IsoId=Q9UKB1-2; Sequence=VSP_006765;
                                                                                                                                                                                                                                                       IsoId=Q9UKB1-1; Sequence=Displayed;
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H-InvDB; HIX0005413; -.
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21-DEC-2004, sequence version 1.
07-FEB-2006, entry version 12.
F-box and WD-40 domain protein 1B (2 days neonate sympathetic ganglion cDNA, RIKEN full-length enriched library, clone:7120487019 product:F-box and WD-40 domain protein 1B, full insert sequence).
Name-Fbxwhb; ORRNames-RP23-94FI1.1-002;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                      121 TALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLIERMVRTDPLWKG
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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MEDQNEDESPKKNTLW (in isoform
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                         /FTId=VSP_006766.
7CD40087EFAA5C8A_CRC64;
                                                                                             Score 2879; DB 1;
Pred. No. 8.3e-205;
0; Mismatches 0;
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RR PETCHET C. P. FUKUSHIMM T., FULNION M., FRUINGER G., FLOWENCE.

RR PETCHET C. P. FUKUSHIMM T., FURNION M., FRUINGER G., GARIBOOTOT.

RR COURSIL-MEMBRING T., FRUINDOM M., FULCKI S., GARIBOIDIG M., GROOTSI-HEMMENT G., GARIBOOTOT.

RR ACTION H., KOLIDAS G., KRISHMAN T., HINCKAWA N., AIMID D., HUMMINGEVIEL, IACONOM M., IKEO V., KILAMUTA H., MIGHORD F., MARCHIONDI L., MACHIBOTOTO M., IKEO C., INDIVIDED S., MORTIS K., MOWILLIAM S., MAGADA BADU M., MAGACE M., MACHIBOTOTO M., IKEO C., ENCOCKAI I. V., LATEAR S., MILL S., MAKANDA S., MILL S., MAKANDA S., MILL S., MAKANDA S., MILL S., MAKANDA S., MILL S., MOWILLIAM S., MAGADA BADU M., MAGACE M., MACHIBOTO F., MACHIBOTO F., MILL S., MOWILLIAM S., MILL S., MOWILLIAM S., MILL S., MAGADA BADU M., MAGACE M., MACHIBOTO F., MILL S., MORTIS K., MOULOGET S., MILL S., M Processor of the control of the cont STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion; MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; STRAIN=C57BL/6J; TISSUE=Sympathetic ganglion; PubMed=16141073; DOI=10.1126/science.1112009; RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium; "Antisense Transcription in the Mammalian Transcriptome."; Science 309:1564-1566(2005). "The transcriptional landscape of the mammalian genome."; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning."; Methods Enzymol. 303:19-44(1999). Science 309:1559-1563(2005). NUCLEOTIDE SEQUENCE. [5] NUCLEOTIDE SEQUENCE NUCLEOTIDE SEQUENCE NUCLEOTIDE SEOUENCE Hayashizaki Y.;

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Ravasi T., Reed J.C., Reed D.J., Reid J. Ringwald M.,
Sandelin A., Schneider C., Semple C.A., Setou M., Shimwada K.,
Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Walls C.,
Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
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A Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
A Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
A Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T.,
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Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
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XX MEDLINE-2108560; PubMed=11217851; DOI=10.1038/3505500;

XB Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

XA Arakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,

A Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Aizawa K., Isawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

XA Actor K., Matsuda H.A., Ashburner M., Batalov S., Casivan T.,

XA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

XA Kuhl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

XA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

A Bronstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M.,

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A Nordone P., Rang B., Ringwald M., Rodriguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Nordone P., Ring B., Ringwald M., Weitz C., Whittaker C., Wilming L.,

Manshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

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Q8K022_MOUSE
Q8K022;
                                                                                  Name=Fbxw11;
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                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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M., Hayashizaki Y.;
(MAR-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                            Prodom; PD000018; WD40; 4.

SMART; SM00256; FB0X; 1.

SMART; SM00320; WD40; 7.

PROSITE; PS00181; FB0X; 1.

PROSITE; PS00678; WD_REPEATS_1; 5.

PROSITE; PS50082; WD_REPEATS_2; 7.

PROSITE; PS50084; WD_REPEATS_2; 7.

PROSITE; PS50024; WD_REPEATS_REGION; 1.

REPEAT; UD1 conjugation pathway; WD repeat.

SEQUENCE 542 AA; 62063 MW; D95A78A6977B828A CRC64;
                                                                                                                                                                                                                                                                                                    99.8%; Score 2872; DB 2;
99.6%; Pred. No. 2.8e-204;
tive 2; Mismatches 0;
                                                            EMBL; AL669951; CAI26097.1; -; Genomic_DNA.
EMBL; AL669844; CAI26097.1; JOINED; GENOMIC_DNA.
EMBL; AL669844; CAI25520.1; -; Genomic_DNA.
EMBL; AL669951; CAI25520.1; -; Genomic_DNA.
EMBL; AL669951; CAI25520.1; -; mRNA.
EMBL; AK149139; BAE28749.1; -; mRNA.
Ensembl; ENSWUSGO0000020271; Mus musculus.
GO; GO:0005512; P:ubiquitin cycle; IEA.
InterPro; IPR001810; F-box.
InterPro; IPR001609; WD40.
                                                                                                                                                            Pfam; PF00646; F-box; 1.
Pfam; PF00400; WD40; 7.
PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 4.
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Best Local Similarity 99.6'
Matches 540; Conservative
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S. I., Wang J., Hsieh F.,

RA Diatchenko L., Maruaina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., BonaldO M.F., Casavant T.L., Scheetz T.B.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratue P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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Richards S., Worley K.C., Shevchenko Y., Bouffact G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffact G.,

Rhiting M., Madan J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Raderation and initial analysis of more than 15,000 full-length human and mouse cunha contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact and contact a
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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SMART; SM00256; FBOX; 1.

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SNART; SM00320; W040; 7.

PROSITE; PS00181; FBOX; 1.

PROSITE; PS00678; WD REPEATS_1; 5.

PROSITE; PS00294; WD REPEATS_2; 7.

PROSITE; PS0294; WD REPEATS_REGION; 1.

Repeat, UD conjugation pathway; WD repeat.

Repeat, UD conjugation pathway; WD repeat.
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Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                   01-OCT-2002, integrated into UniProtKB/TrEMBL 01-OCT-2002, sequence version 1.
PFBB-2006, entry version 22.
P-box and WD-40 domain protein 11.
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HSSP; Q9Y297; 1P22.
Ensembl; ENSWIGS000000202271; Mus musculus.
MGI; MGI:2144023; Pbxw11.
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ProDom; PD000018; WD40; 4.
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PRELIMINARY;
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Pfam; PF00400; WD40; 7.
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QBBY90 MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-2001, sequence version 1.
01-DEC-2001, sequence version 1.
07-FBB-2006, entry version 22.
F-box/WD40 repeat-containing protein HOS.
Name=Fbxw11; Synonyme=Fbxw1b;
Mus musculus (Mouse).
Bukaryocis (Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Murcidea; Muridae; Murinae; Mus.
                                                                                                                                 CHYQHGHINSYLKPMLQRDFITALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVIS
                                                                                                                                                                                                                                                                                                                                                           MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLQSMPSVRCLQNTSVMEDQNED
                                       -----QISNGTSSVIVSRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISRM
                                                        ESPKKSALWQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISRM
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                                                                                                                                                                                                          EGMLWKKLIERWVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKIIQDIETI
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                                                                                                                                                                                                                                                                                  TGSVLCLQYDERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKD
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STRAIR=FVB/N;
STRAIR=FVB/N;
MEDLINE=21906231; PubMed=11896578; DOI=10.1038/sj.onc.1205311;
MEDLINE=21906231; PubMed=11896578; DOI=10.1038/sj.onc.1205311;
Bhatia N., Herter J.R., Slaga T.J., Fuchs S.Y., Spiegelman V.S.
"Mouse homologue of HOS (mHOS) is overexpressed in skin tumors implicated in constitutive activation of NF-kappaB.";
Oncogene 21:1501-1509(2002).
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Ensembl; BNSWUSG000020271; Mus musculus.
MGG1, MG1:2144023; FDXw11.
GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPR001810; F-box.
InterPro; IPR001680; W040.
Pfam; PF00646; F-box; 1.
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HSSP; Q9Y297; 1P22.
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3 days neonate thymus cDNA, RIKEN full-length enriched library, clone.A630019111 product:F-BOX/WD-REPEAT FROTEIN 1B (F-BOX AND WD-REPEATS PROTEIN BETA-TRCP2) honolog (F-box and WD-40 domain protein 1B) (Bone marrow macrophage cDNA, RIKEN full-length enriched library, clone:I830054811 product:F-box and WD-40 domain protein 1B, full
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Manae-Ebxablo, Synonyms-Fbxwll; ORFNames=RP23-94F11.1-001;
Mus musculus (Mouse)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
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PROSITE; PSO0678; WD REPEATS 1; 5.
PROSITE; PSSO0824; WD REPEATS 2; 7.
PROSITE; PSC0294; WD REPEATS REGION; 1.
Repeat; Ubl conjugation pathway; WD repeat.
SEQUENCE 563 AA; 64742 MW; 9AB562F3FF5E3496 CRC64;
                                                                                                                                                                                                                                            Score 2755.5; DB 2;
Pred. No. 1.3e-195;
2; Mismatches 15;
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01-MAR-2003, sequence version 1.
07-FEB-2006, encry version 24.
3 days neonate thymus cDNA, RIKEN full-length
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                 PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 4.
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Matches 525; Conservative
                                         ProDom; PD000018; WD40; 4
SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
WD40; 7.
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RA Ambesi-Impionate A. Apwailer R. Aturaliya R.N., Balley T.L.,

Bansal M. Baxter L. Beisel K.W. Bersano T., Bono H., Chalk A.M.,

RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,

Gine Bernardo D., Down T., Engerrom P., Fagiolini M., Faulkner G.,

RA Georgii-Hemming P., Gingerson P., Fagiolini M., Faulkner G.,

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RA Hill D., Huminitecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,

RA Hill D., Huminitecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,

RA Kirano H., Kollias G., Katchnan S.P., Kruger A., Kummerfeld S.K.,

RA Kurdaki H., Masusawa S., Miki H., Mignone F., Miyake S., Morris K.,

Luni S., Marbura S., Madan Babu M., Madera M., Marchionni L.,

Mutagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,

RA Matsuawa S., Miki H., Mignone F., Miyake S., Morris K.,

RA Matsuawa S., Mikhawa S., Nori F., Ohara O.,

RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,

Rott B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,

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Rammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Takanaka Y., Takinaka Y.,

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Rawashima T., Watanaki Y., Watahiki A., Okamura-Oho Y., Shiraki T., Suzuki J.,

Rawashizahi Y., Shiraka S.,
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                                                                                                                    STRAIN=CSTBL/67; TISSUE=Bone marrow, and Thymus; MEDLINE-99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9; Carninci P., Hayashizaki Y.; Hajashizaki Y.; High-efficiency full-length cDNA cloning."; Methods Enzymol. 303:19-44(1999).
Mammalia; Butheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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                                                                                                                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUB=Bone marrow, and Thymus;
PubMed=16141072; DOI=10.1126/science.1112014;
                           Muridae; Murinae; Mus
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                              Muroidea;
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Ranal R., Murchkin I.V., Lew Y., Lenhard B.i. Dyona N.A.;
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Ranal R., Murchenka Y., Taylor R.S., Taesdala B. R., Ringwald M.,
Sandellin A., Schmeider C., Semple C.A., Secon M., Shanda K.,
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Ranal R., Marki K., Kasal Y., Simmer A., Carninci P. Haytan W.,
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Ranure G., Toward M., Macescon R., Jahbita K., Itahia Y., Itoh M., Kagawa I.,
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Ranure G., Toward Y., Weshino M., Andhura W., Machina R., Markin R.,
Ranure G., Toward Y., Weshino M., Andhura W., Manil M., Machina M., Machi

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LQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVW
                                                                                                                                                                                                                                                                                   full insert sequence
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NUCLEOTIDE SEQUENCE.
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                                                                             Σ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QISNGTSSVIVSRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHIN
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                                                                                                                                                                                                                                                          STRAIN=CSTBL/6J; TISSUE=Bone marrow; Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hori F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S., Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N., Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D., Shibata K., Shizaki T., Tagami M., Tagami Y., Waki K., Watahiki A., Submitted (MAR*2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.6%; Score 2665.5; DB 2; Length 529; 92.4%; Pred. No. 5.6e-189; ive 4; Mismatches 1; Indels 37;
                                                                                                                                                                                                                       to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AK041532; BAC310975.1; -; mRNA.
EMBL, AL669844; CAI25519.1; -; Genomic_DNA.
EMBL, AL669951; CAI25519.1; JOINED; GENOMIC_DNA.
EMBL, AL669951; CAI26099.1; -; GENOMIC_DNA.
EMBL, AL669944; CAI26099.1; JOINED; GENOMIC_DNA.
EMBL, AKIS2181; BAE31012.1; -; mRNA.
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les 512; Conservative
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                                                                                                                                                                     DLQAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFLNVPPSAQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=Fbxwll;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IISSUE=Mammary gland;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-FEB-2006, entry version 6.
Mammary gland RCB-0526 Jyg-MC(A) cDNA, RIKEN full-length enriched
library, clone:G830018H24 product:F-box and WD-40 domain protein 1B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Mammary gland;
PubMed=16141072; DOI=10.1126/science.1112014;
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Methods Enzymol. 303:19-44(1999).
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Q3TLZ8;
                                                                                                                                                                                                                                                                                                     ETRSPSRTYTYISR 542
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NUCLEOLIDE SUCCEASION.

REDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

MEDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

MEDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

MEDLINE-22354683; PubMed=12466851; DOI=10.1038/nature01266;

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                                                                                                                                                                                                                             TISSUE=Mammary gland;
PubMed=16141073; DOI=10.1126/science.1112009;
RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
"Antisense Transcription in the Mammalian Transcriptome.";
Science 309:1564-1566(2005).
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                                                                                                                 The transcriptional landscape of the mammalian genome.";
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MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                  Science 309:1559-1563(2005)
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Nature 409:685-690(2001). NUCLEOTIDE SEQUENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
TISSUE=Mammary gland;
MEDLINE=20499374; Publed=11042159; DOI=10.1101/gr.145100;
MEDLINE=20499374; Publed T. Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Konno H., Okazaki T., Muramatsu M., Hayashizaki Y.;
Mormalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                    MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibara K., Titch M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsunioto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Riki integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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PROSITE; PS00678; WD_REPEATS_1; 5.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
Repeat; UD! conjugation pathway; WD_repeat.
SEQUENCE 529 AA; 60799 MW; CE035C809824D472 CRC64;
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MGI; MGI:2144023; FDxw11.
GO; GO:0006512; P:ubxquitin cycle; IEA.
InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
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SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
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Pfam; PF00400; WD40; 7.
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11-0CT-2005, sequence version 1.
11-0CT-2005, sequence version 1.
11-0CT-2005, sequence version 6.
17 days embryo kidney cDNA, RIKEN full-length enriched library, clone:1920043C06 product:F-box and WD-40 domain protein 1B, full insert sequence (Osteoclas-like cell cDNA, RIKEN full-length enriched library, clone:1420048G02 product:F-box and WD-40 domain protein 1B, full insert sequence).
Mus musculus (Mouse).
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NLORIOCRSENSKGVYCLOYDDEKIISGLRDNSIKIWDKTSLECLKVLTGHTGSVLCLQY
                 216 NLQRIQCRSENSKGVYCLQYDDDKIISGLRDNSIKIWDKSSLECLKVLTGHTGSVLCLQY
                                                                 DERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAVWDMA
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Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
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                                                                                                                                                                                                                   STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazati Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
          Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazarelli J., Monbaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Carninci P., de Bonaldo M.F.,
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SMART; SM00320; WD40; 7.

PROSITE; PSS0181; FBOX; 1.

PROSITE; PS0678; WD REPEATS 1; 5.

PROSITE; PS50082; WD_REPEATS 2; 7.

PROSITE; PS50294; WD_REPEATS_REGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AK168667; BAE40519.1; -; mRNA.
EMBL; AK160086; BAE55617.1; -; mRNA.
GO; GO:0006512; P:ubiquitin cycle; IEA.
INCEPED: IPR001810; F-box.
InterPro; IPR001680; WD40.
Bojunga N.,
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Pfam; PF00400; WJ01; 7.
PRINTS; PR00320; GPROTEINBRPT.
ProDom; PD000018; WD40; 4.
., Boffelli D.,
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                                                                                                                                                                                                      SEQUENCE
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAVWDWASATDITLRRVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 RKRPSEGNYQKEKDLCIXYFDQMSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFI
                                                                                                                           1 MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLQSMPSVRCLQISNGTSSVIVS
                                                                                                                                                               SVIVST----ISNGTSSVIVS
                                                                                                                                                                                                                                    27 RKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFI
                                                                                                                                                                                                                                                                          121 TALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLIERMVRTDPLWKG
                                                                                                                                                                                                                                                                                                                                             LSERRGWDQYLFKNRPTDGPPNSFYRSLYPKIIQDIETIESNWRCGRHNLQRIQCRSENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GHRAAVNVVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQYRDRLVVSGS
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                        Gaps
                                                                                        34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Brain;
Okazaki N., Kikuno R., Ohara R., Inamoto S., Hara Y., Nagase
Ohara O., Koga H.;
                                                      Length 508;
                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
conjugation pathway; WD repeat.
                                                                         .4e-188;
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                                                      92.4%; Score 2660; DB 93.4%; Pred. No. 1.4e-1
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                                                                     Pred. No. 1.4e
2; Mismatches
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Mus musculus (Mouse).
                                                                                                                                                  EMBL; AB093260; BAC41444.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2003, sequence version 1.
21-FEB-2006, entry version 21.
MKIAA0696 protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                         Local Similarity 93.4 es 506; Conservative
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                      508 AA;
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                      SEQUENCE
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SPIDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIAC 395
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                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ERMYRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPKIIQDIETIESNWRCGRH
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             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                              STRAIN-CB; TISSUE-Bursa;
Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J.,
Fiedler P., Kutrer S., Blagodatski A., Kostovska D., Koter M.,
Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.;
"Full-length cDNAs from chicken bursal lymphocytes to facilitate
                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
PROSITE; PS50181; FBOX; 1.
PROSITE; PS0082; WD_REPEATS 1; 5.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_REGION; 1.
Hypochetical protein; Repeat; Ubl conjugation pathway; WD repeat.
SEQUENCE 529 AA; 60924 WW; 0DCD9905FSD0F1E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2652.5; DB 2; Length 529;
Pred. No. 5.1e-188;
2; Mismatches 6; Indels 37;
                                                                                                                                                                                                                                                                                                EMBL, AJ721075, CAG32734.1, -; mRNA.
GO; GO:0006512, P:ublqquitin cycle; IEA.
InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
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Pfam; PF00400; WJ00; 7.
PRINTS; PR00320; GPROTEINBRPT.
Probom; PD000018; WD40; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.1%;
91.9%;
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Genome Biol. 6:R6-R6(2005)
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Best Local Similarity 91.9
Matches 509; Conservative
 (Chicken).
                                                                 NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                      555;
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                                                                                                                                                                                                                                                                                                                     Length
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                                                                                                                                                                                                                                                                                                                     Score 2660; DB 2;
Pred. No. 1.5e-188;
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                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
HSSP; Q9Y297; 1P22.
Ensembl; ENSWMGS0000020271; Mus musculus.
MGI; MGI:2144023; Pbxw11.
InterPro; 1PR001810; F-box.
InterPro; 1PR001810; F-box.
InterPro; 1PR00180; WD40.
Pfam; PF00646; P-box; 1.
PRINTS; PR00320; GPROTEINBRPT.
PRODOM; PD000018; WD40; 7.
PRINTS; SW00256; FBOX; 1.
SWART; SW00256; FBOX; 1.
PROSITE; PSS0181; FBOX; 1.
PROSITE; PSS0181; FBOX; 1.
PROSITE; PSS0039; WD_REPEATS_1; 5.
PROSITE; PSS0039; WD_REPEATS_2; 7.
PROSITE; PSS00294; WD_REPEATS_2; 7.
PROSITE; PSS0294; WD_REPEATS_RGION; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           555 AA; 63288 MW;
                                                                                                                                                                                                                                                                                                                     92.4%;
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nes 506; Conservative
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NON TER
SEQUENCE
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Q5 ZHQ9 Q5
ID Q5Z
AC Q5Z
DT 23-
DT 23-
DT 07-
DB HYE
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155

275 348

Gaps

19;

61 46 121

241

181

346

286

301

466

481

406

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VRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLVG 361
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MEDLINE=98325370; PubMed=8660940; DOI=10.1016/S1097-2765(00)80056-8;
Margottin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                        SERRGWDQYLFKNRPTDGPPNSFYRSLYPKIIQDIETIESNWRCGRHNLQRIQCRSENSK
                                                                                                                                                                                                                                                                                                                                                        242 GVYCLQYDDEKIISGLRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDST
                                                                                                                                                                                                                                                                                                                                                                          227 GVYCLQYDDEKIISGLRDNSIKIWDKQTLECLKILTGHTGSVLCLQYDERVIVTGSSDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347 HRAAVNVVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSS
                                                                                                                                          KRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFIT
                                                                                                                                                                                                                ALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLIERMVRTDPLWKGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRAAVNVVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPAS
                                                                     7 IEDKTIELMCSVPRSLWLGCANLVESMCA----LSCLQSMPSVRCLQISNGTSSVIVSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-FEE-2001, integrated into UniProtKB/Swiss-Prot. 01-NOV-1999, sequence version 1. 07-FEE-2006, entry version 52. F-borKB-2006, entry version 52. F-borKMD-repeat protein 1A (F-box and WD-repeats protein beta-TrCP) (E3RSTKappaB) (pikappaBalpha-E3 receptor subunit). Name-BTRC; Synonyms-BTRCP, FBW1A, FBXW1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [MRN4] (ISOFORM 1).
MEDLINE=99075339; PubMed=885996; DOI=10.1038/25159;
MAZON A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M., Andersen J.S., Mann M., Marcurio F., Ben-Neriah Y.;
"Identification of the receptor component of the IkappaBalpha-
 DB 2; Length 527;
                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deember 10
 85.0%; Score 2448.5; DB 2;
86.1%; Pred. No. 7e-173;
ive 30; Mismatches 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ubiquitin ligase.";
Nature 396:590-594(1998).
Query Match
Best Local Similarity 86.1
Matches 466; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
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Q9Y297; Q9Y213;
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"Generation and initial analysis of more than 15,000 full-length human
   DLQAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFLNVPPSAPN 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                         brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSSO181; FBOX; 1.
PROSITE; PSO0678; WD REPEATS 1; 5.
PROSITE; PSS0082; WD REPEATS 2; 7.
PROSITE; PSC0294; WD REPEATS REGION; 1.
Repeat; Ubl conjugation pathway; WD repeat.
SEQUENCE 527 AA; 60547 MW; 563F3C014CA099C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                   05-JUL-2004, integrated into UniProtKB/TrEMBL
                                                                                                                                                                  527 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ensembl; ENSDARGO000017230; Danio rerio.
ZFIN, ZDB-GENE-040456-2903; zgc:63728.
GO, GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPR001810; F-box.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BC056809; AAH56809.1; -; mRNA.
                                                                                                                                                                  PRT;
                                                                                                                                                                                                                   05-JUL-2004, sequence version 1. 07-FEB-2006, entry version 17.
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ProDom; PD000018; WD40; 4.
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                                                                                                                                                              QEPGW4_BRARE PRELIMINARY;
Q6PGW4;
                                      and mouse cDNA sequences."
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Pfam; PF00400; WD40; 7.
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SMART; SM00320; WD40; 7.
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NCBI_TaxID=7955;
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ubiquitination of proteins involved in cell cycle progression,
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WD 3.
WD 4.
WD 5.
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ProDom; PD000018; WD40; 4.
SMART; SM00256; FBOX; 1.
SMART; SM00320; WD40; 7.
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Pfam; PF00400; WD40; 7.
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PROSITE; PS00678; WD REI
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                                                                                                                                                                                                                      Name=2
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TURN
     MEDLINE=22388257; PubbMed=12477922; DOI=10.1073/pnas.242601899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Alausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Alpokins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Scheetz T.B., Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Rokama P.J., McKernan K.J., Malek J.A., Ghap L.J., Hulyk S.W., Nilalon D.K., Murny D.M., Sodergren B.J., Lu X., Glibbs R.A., Whiting M., Maden A., Young A.C., Shevchenko Y., Bouffard G.G., Ahiting M., Maden A., Young A.C., Shevchenko Y., Bouffard G.G., Antiting M., Maden A., Young A.C., Shevchenko Y., Bouffard G.G., Abrance A.C., Grimwood J., Schwutz J., Myers R.M., Butkefley R.W., Touchman J.W., Green E.D., Dickson M.C., Shebell Y.S.N., Xrzywinski M.I., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA scrience.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ligase.";
Mol. Cell 11:1445-1456(2003).
-!- FUNCTION: Substrate-recognition component of the SCF (SKP1-CUL1-F--box protein) ubiquitin ligase complex, which mediates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.95 ANGSTROMS) OF 175-605 IN COMPLEX WITH SKP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22706071; PubMed=12820959; DOI=10.1016/S1097-2765(03)00234-X; Mu G., Xu G., Schulman B.A., Jeffrey P.D., Harper J.W., Payletich N.P.; Structure Of a beta-TrCP1-8kp1-beta-catenin complex: destruction motif binding and lysine specificity of the SCF(beta-TrCP1) ubiquitin
Thomas D., Strebel K., Benarous R.; "A novel human WD protein, h-beta TrCp, that interacts with HIV-1 Vpu connects CD4 to the ER degradation pathway through an F-box motif."; wol. Cell 1:565-574(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=B-cell;
MEDLINE=20437281; PubMed=10983987; DOI=10.1016/S1097-2765(00)00040-X;
MEDLINE=20437281; PubMed=10983987; DOI=10.1016/S1097-2765(00)00040-X;
Kleijnen M.F., Shih A.H., Zhou P., Kumar S., Soccio R.E.,
Kedersha N.L., Gill G., Howley P.M.;
"The hDLIC picteins may provide a link between the ubiquitination machinery and the proteasome.";
Machinery and the proteasome.";
Mol. Cell 6:409-419(2000).
                                                                                         NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM 2).
MEDLINE=20003060; PubMed=10531035; DOI=10.1016/S0960-9822(00)80020-2;
Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harper J.W.;
"The SCF(beta-TRCP) ubiquitin ligase complex associates specifically with phosphorylated destruction motifs in I-kappa-B-alpha and betacenin and stimulates I-kappa-B-alpha ubiquitination in vitro."; Genes Dev. 13:270-283(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=22072105; PubMed=12077367; Sadot E., Conacci-Sorrell M., Zhurinsky J., Shnizer D., Lando Z., Zharhary D., Kam Z., Ben-Ze'ev A., Geiger B.; Tregulation of 833/837 phosphorylated beta-catenin in normal and transformed cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99145464; PubMed=9990852;
Winston J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,
                                                                                                                                                            "Identification of a family of human F-box proteins."; Curr. Biol. 9:1177-1179(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERACTION WITH UBOLN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHARACTERIZATION.
                                                                                                                                                 Pagano M.;
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PROSITE; PS00629; WD_REPEATS_2; 7.
PROSITE; PS50094; WD_REPEATS_EGION; 1.
3D-structure; Alternative splicing; Ligase; Polymorphism; FUbl conjugation pathway; WD repeat; Wnt signaling pathway. CHAIN 1 605 F-box/WD-repeat procein 1A.
DOMAIN 190 228 F-box.
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A -> S (in dbSNP:4151060)
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P -> H (in dbSNP:2270439)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=09Y297-2; Sequence=VSP_006764;
-!- SIMILARITY: Contains 1 F-box domain.
-!- SIMILARITY: Contains 7 WD repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=09Y297-1; Sequence=Displayed;
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EMBL; Y14153; CAA74572.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AF129530, AAF04464.1, -; mRNA.
EMBL, BC027994, AAH27994.1, -; mRNA.
PDB, 1P22; X-ray; A=175-605.
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SRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDF 119
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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SMART; SM00256; FBOX; 1.
SMART; SM00320; WH040; 7.
PROSITE; PSS00678; WD_REPEATS_1; 6.
PROSITE; PSS00678; WD_REPEATS_1; 6.
PROSITE; PSS0082; WD_REPEATS_2; 7.
REPEAT; UB! CONJUGATION PATHWAY; WD_REPATS_REGION; 1.
SEQUENCE 605 AA; 68867 MW; 4C67P3B7E400FD37 CRC64;
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EMBL; AL445463; CAH70020.1; JOINED; Genomic_DNA.
EMBL; AL62444; CAH70020.1; JOINED; Genomic_DNA.
EMBL; AL64463; CAI12663.1; -; Genomic_DNA.
EMBL; AL627424; CAI12963.1; -; Genomic_DNA.
EMBL; AL627424; CAI12963.1; JOINED; Genomic_DNA.
EMBL; AL627424; CAI41042.1; -; Genomic_DNA.
EMBL; AL627434; CAI41042.1; -; Genomic_DNA.
EMBL; AL645463; CAI41042.1; -; Genomic_DNA.
EMBL; AL64563; CAI41042.1; JOINED; Genomic_DNA.
ENSEMD!, ENSGO0000156167; Homo sapiens.
GO; GO:0006512; P:ubiquitin cycle; IEA.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84.9%; Score 2445.5; DB 2; 75.7%; Pred. No. 1.4e-172; iive 49; Mismatches 35;
                                                                                                                                                                         10-MAY-2005, integrated into UniProtKB/TrEMBL. 10-MAY-2005, sequence version 1. 07-FBE-2006, entry version 11. 07-FBE-2006, entry version 11. Name-arransducin repeat containing. Name-ETRC; ORFNames=RP11-529110.2-001;
                                                                                                                                      PRT;
                                                                                                                                        QSW141_HUMAN PRELIMINARY;
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Pfam; PF00400; WD40; 7.
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  538 TYISR
                                   601 TYISR
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Best Local Simi
Matches 458;
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75.7%; Pred. No. 1.4e-172;
tive 49; Mismatches 35;
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nes 458; Conservative
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GLAERRGWGQYLFKNKPPDGNAPPNSFYRALYPKIIQDIETIESWWRCGRHSLQRIHCRS
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                                                             ITALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLIERMVRTDPLWK
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CS7BL/6J;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
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11-OCT-2005, sequence version 1.
11-OCT-2006, entry version 6.
Blastocyst blastocyst cDNA, RIKEN full-length enriched library, clone: IICO023312 product:beta-transducin repeat containing protein,
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PubMed=16141072; DOI=10.1126/science.1112014;
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"High-efficiency full-length cDNA cloning.";
Methods Enzymol. 303:19-44(1999).
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Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,

RA Hill D., Huminlecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,

RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,

RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,

RA Kitano H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,

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RA Mottagui-Tabar S., Mider N., Nakano M., Makauchi H., Mg P.,

RA Milsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara G., Pesole G.,

RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara G., Pesole G.,

RA Roazaki Y., Orlando V., Salzberg S.L., Sandelin A., Schneider C.,

Rober B., Kuan Y., Salzberg S.L., Sandelin A., Schneider C.,

RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,

RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,

Schonbach C., Sekiguchi K., Semple C.A., Sano S., Sessa L., Sheng Y.,

RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,

RA Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,

RA Tammoja K., Tan S.L., Taylor M.S., Zimmer A., Hide W., Bult C.,

RA Ananishii H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,

RA Mahlestedt C., Mattick M.D., Liu E.T., Brusic V., Quackenbush J.,

R. Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,

R. Inamura K., Itoh M., Kato T., Kawaji H., Kawashira N.,

R. Hayashira T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,

R. Tagami M., Pakashira H., Nakano K., Shiraki Y.,

R. Tagami M., Pakashira H., Rawashina J.,

R. Tagami M., Pakashira H., Rawashina J.,

R. Tagami M., Pakashira K., Shiraki Y.,

R. Tagami M., Pakashira H., Shiraki Y.,

R. Tagami M., Pakashira H., Kawashina J.,

R. Tagami M., Pakashira H., Watahiki M., Okamura-Oho Y., Suzuki H., Kawashina J.,

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              Kawai J. Shinagawa A., Shibata K., Yoshino M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Itoh M., Kondo H., Kaankawa T., Saito T., Orazaki Y., Gojobori T., Bono H., Kaankawa T., Saito R., Matsuda H., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H., Sasto T., Saito R., Nakaido I., Pesole G., Quackenbush J., Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Magner L., Washlo T., Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Lyons P., Marchionni L., Mashima J., Manzarelli J., Mombaetts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Storch K.-F., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Wynshaw Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hashahzaki Y., Rawai Y., Kawaji H., Pannari M., Handella M., Hashahzaki Y., Rodriki S., Hashahzaki Y., Rawai Y., Kawaji H., Pannari M., Handella M., Handella M., Handella M., Handella M., Handella M., Handella M., Kawaji H., Kohtsuki S., Handella M., Handella M., Kawaji H., Kantaki Y., Landella M., Handella M., Kawaji H., Kantaki Y., Kawaji H., Handella M., Handella M., Kawaji H., Kantaki Y., Landella M., Handella M., Handella M., Kawaji H., Kantaki Y., Landella M., Handella M., Handella M., Handella M., Handella M., Kawaji H., Handella M., Han
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new genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIDLINE-20530913; PubMed=11076861; DOI=10.1101/gr.152600; Shibara K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Itoh M., Aizawa K., Nagaoka S., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Riki integrated sequence and Y., Kira A., Hayashizaki Y.; RIKE integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CS7BL/6J;

MEDLINE-20499374; PubMed=11042159; DOI=10.1101/gr.145100;

Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;

Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
eenome Res. 10:1617-1630(2000).
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MG1; MG1:1338871; Btrc.
GO; GO:0005789; C:endoplasmic reticulum; RCA.
GO; GO:0006484; F:ubiquitin conjugating enzyme activity; RCA.
GO; GO:0006464; P:protein modification; RCA.
GO; GO:000611; P:ubiquitin-dependent protein catabolism; RCA.
InterPro; IPR001810; F-box.
InterPro; IPR00180; WD40.
Pfam; PF00646; F-box; 1.
   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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Pfam; PF00400; WD40; 7.
PRINTS; PR00320; GPROTEINBRPT.
Probom; PD000018; WD40; 4.
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SMART; SM00320; WD40; 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          241 GLAERRGWGQYLFKNKPPDENAPPNSFYRALYPKIIQDIETIESNWRCGRHSLQRIRCRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ETSKGVYCLQYDDQXIVSGLRDNTIKIWDKSTLECKRILTGHTGSVLCLQYDERVIITGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=Btrc; Synonyms=mXIAA4123;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Musinae; Mus
                                                                                                                                                                                                                       60 SRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 GLSERRGWDQYLFKNRPTD - GPPNSFYRSLYPKIIQDIETIESNWRCGRHNLQRIQCRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPR
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                                                                                                                                                                                                                                                                        40 -----OSMPSVRCL---QISNGTSSVIV
                                                                                                                                                                Gaps
                                                                                                                                                                63;
                                                                                                                              2; Length 605;
                                                                                                                                                                Indels
                                                                                          557B3942F52DC472 CRC64;
                                                                                                                                                                                                  1 MEP-DSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCL
                                                                                                                            Query Match 84.7%; Score 2437.5; DB 2; Best Local Similarity 75.4%; Pred. No. 5.5e-172; Matches 456; Conservative 51; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-MAY-2005, integrated into UniProtKB/TrEMBL
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                                                                           repeat
PROSITE; PS50181; FBOX; 1.
PROSITE; PS00678; WD_REPEATS_1; 6.
PROSITE; PS50082; WD_REPEATS_2; 7.
PROSITE; PS50294; WD_REPEATS_EGION; 1.
Repeat; Ubl conjugation pathway; WD repsecut; Ubl conjugation pathway; WD repsecutor
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21-FEB-2006, entry version 10.
MKIAA4123 protein (Fragment).
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TISSUE=Brain;
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Q571K6;
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Homo sapiens (Human)
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                                                                                 TYISR 542
                                                                                                                                                                                                                                                                                                  Name=DKFZp781N011;
                                                                                                              TYISR 639
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
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QEBDSO;
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                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
             Saga Y., Nagase T., Ohara O., Koga H.;
"Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene. The Complete Nucleotide Sequences of Mouse KIAA-homologous cDNAs Genetified by Screening of Terminal sequences of cDNA Clones Randomly Sampled from Size-Fractionated Libraries. "; Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
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Inamoto S., Koseki H., Hiraoka S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84.6%; Score 2436.5; DB 2; Length 639; 75.4%; Pred. No. 7e-172; cive 50; Mismatches 36; Indels 63;
                                                                                                                                                                             EMBL; AK220183; BAD90368.1; -; mRNA.
Ensembl; ENSWUSG0000025217; Mus musculus.
MGI:1338871; Btrc.
GO; GO:0005783; C:endoplasmic reticulum; RCA.
GO; GO:0004840; F:ubiquitin conjugating enzyme activity; RCA.
GO; GO:0006464; P:protein modification; RCA.
GO; GO:0000511; P:ubiquitin-dependent protein catabolism; RCA.
InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
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Ffam: PF00400; WD40; 7.

PRINTS; PR00320; GPROTEINBRPT.

SMART; SW00326; FBOX; 1.

SMART; SW00320; WD40; 7.

PROSITE: PS50181; FBOX; 1.

PROSITE: PS50083; WD_REPEATS_1; 6.

PROSITE: PS50083; WD_REPEATS_2; 7.

PROSITE: PS50083; WD_REPEATS_REGION; 1.
 Okazaki N., Kikuno R.F., Ohara R.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYQHGHINSYLKPMLQRDFITALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISE 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homo saptens inuman).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae;
                             GMLWKKLIERMVRTDPLWKGLSERRGWDQYLFKNRPTDG--PPNSFYRSLYPKIIQDIET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APASTLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFLNVPPSAQNETRSPSRTY
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Pfam; PF00400; WD40; 7.

PRINTS; PR00320; GPROTEINBRPT.

PRODOUG; WD40; 4.

SMART; SM00226; FBOX; 1.

SMART; SM00326; FBOX; 1.

PROSITE; PS00678; WD REPEATS_1; 6.

PROSITE; PS00678; WD REPEATS_1; 6.

PROSITE; PS0069; WD REPEATS_1; 7.

PROSITE; PS00294; WD REPEATS_ROJO; 1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Amygdala;
The German cDNA Consortium;
The German cDNA Consortium;
Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osar
Fobo G., Han M., Wiemann S.;
Submitted (AUG-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84.5%; Score 2434; DB 2;
80.5%; Pred. No. 9.1e-172;
ive 41; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                          11-OCT-2004, integrated into UniProtKB/TrEMBL.
11-OCT-2004, sequence version 1.
07-FEB-2006, entry version 11.
Hypochetical protein DKFZp781N011.
                                                                                                                                                                                                                                                                                                         564 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, CR749295, CAH18150.1, -; mRNA.
Ensembl, ENSG0000166167, Homo sapiens.
GO, GO:0006512, P:ubbaquitin cycle; IEA.
InterPro; IPR001810; F-box.
InterPro; IPR001680; WD40.
                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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HTGSVLCLQYDERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSK 338
                                         DRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTSTCEFVRT 398
                                                              LNGHKRGIACLOYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVS 458
                                                                                    FLNVPPSAQNETRSPSRTYTYISR 542
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                 $ B $ B $ B $ B $
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Search completed: August 25, 2006, 07:22:29 Job time : 307 secs

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GenCore version 5.1.9 (c) 1993 - 2006 Biocceleration Ltd.
                  Copyright
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OM protein - protein search, using sw model

August 25, 2006, 07:22:47 ; Search time 50 Seconds Run on:

(without alignments) 948.832 Million cell updates/sec

US-10-665-715-16 2879

1 MEPDSVIEDKTIELMCSVPR......PPSAQNETRSPSRTYTYISR Title: Perfect score:

542

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

650591 segs, 87530628 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/EMC\_Celerra\_SIDS3/ptodata/2/iaa/5\_COMB.pep:\*
/EMC\_Celerra\_SIDS3/ptodata/2/iaa/6\_COMB.pep:\*
/EMC\_Celerra\_SIDS3/ptodata/2/iaa/7\_COMB.pep:\*
/EMC\_Celerra\_SIDS3/ptodata/2/iaa/T\_COMB.pep:\*
/EMC\_Celerra\_SIDS3/ptodata/2/iaa/TCOMB.pep:\*
/EMC\_Celerra\_SIDS3/ptodata/2/iaa/RCOMB.pep:\*
/EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\*
/EMC\_Celerra\_SIDS3/ptodata/2/iaa/RE\_COMB.pep:\* Issued Patents AA:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Appl	, Appl	Appli	Appli	, Appl	, Appl	, Appl	, Appl	, Appl	, Appl	Appli	, Appl	Appli	, Appl	Appli	Appli	Appli	Appli								
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Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
ID	US-09-832-161-16	US-09-832-161-18	US-09-385-219A-2	US-09-601-168B-2	US-08-190-802A-30	US-08-477-346-30	US-08-473-089-30	US-08-487-072A-30	US-09-213-888-21	US-09-328-877D-21	US-09-213-888-7	US-09-213-888-10	US-09-328-877D-7	US-09-328-877D-10	US-09-213-888-6	0	US-09-213-888-5	0	US-09-213-888-9	-09-328-	US-09-213-888-8	-09-328-	US-09-213-888-4	-09	1	US-09-328-877D-3
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* Query Match	100.0	82.8	82.8	82.8	79.4	79.4	79.4	79.4	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3	22.3
Score	2879	2384.5	2384.5	2384.5	2286.5	2286.5	2286.5	2286.5	643	643	641.5	641.5	641.5	641.5	641.5	641.5	641.5	641.5	641.5	641.5	641.5	641.5	641.5	641.5	641.5	641.5
Result No.	-	8	m	4	S	9	7	80	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	4 25	26

Sequence 27, Appl Sequence 25, Appl Sequence 25, Appl Sequence 314, App Sequence 30, Appl Sequence 31, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 32, Appl Sequence 34, Appl Sequence 264, Appl Sequence 264, Appl Sequence 18953, A Sequence 31, Appli Sequence 31, Appli
US-09-213-888-27 US-09-13-888-27 US-09-13-888-25 US-09-328-877D-25 US-09-487-558B-314 US-09-177-165A-30 US-08-177-165A-30 US-08-177-165A-30 US-08-477-346-32 US-08-477-346-32 US-08-477-346-32 US-08-477-346-32 US-08-477-346-32 US-08-477-346-32 US-08-477-346-32 US-08-477-346-32 US-08-477-346-32 US-08-477-346-32 US-08-478-99-8 US-09-538-092-264 US-08-288-917-3 US-08-288-917-3 US-08-288-917-3 US-08-281-716-3
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## ALIGNMENTS

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181 LSERRGWDQYLFKNRPTDGPPNSFYRSLYPKIIQDIETIESNWRCGRHNLQRIQCRSENS 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 RKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWRKLIERMVRTDPLWKG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 KGVYCLQYDDEKIISGLRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLIERMVRTDPLWKG 180
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                                                           APPLICANT: Manning, Anthony M.
APPLICANT: Manning, Anthony M.
APPLICANT: Manning, Anthony M.
APPLICANT: Manning, Sharon
APPLICANT: Amit, Sharon
APPLICANT: Ben-Neriah, Yinon
APPLICANT: Lavon, Iris
APPLICANT: Hatzubai, Ada
APPLICANT: Hatzubai, Ada
APPLICANT: Hatzubai, Ada
APPLICANT: Arcan, Avraham
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
TITLE OF INVENTION: NP-kB
TITLE OF INVENTION: NP-kB
TITLE OF INVENTION: NP-kB
TITLE OF INVENTION NUMBER: US/09/832,161
CURRENT APPLICATION NUMBER: 09/210,060
PRIOR APPLICATION NUMBER: 09/210,060
PRIOR PLING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 542
TYPER: PRI
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Sequence 16, Application US/09832161; Patent No. 6656713; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Homo sapiens
US-09-832-161-16
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94 HLISRMCHYQHGHINSYLKPMLQRDFITALPEQGLDHIAENILSYLDARSLCAAELVCKE 153
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299 CKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNG 358
                                                                                                                     391
                                                                                                                                                                                     451
                                                      331
                                                                                                                                                                                                                                                                     61 S--TAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            212 IIQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISGLRDNSIKIWDKTSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---VP----RSLWLGCANLV---ESMCAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37 SCLQSMPSVRCL---QISNGTSSVIVSRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 WQRVISEGMLWKKLIERMVRTDPLWKGLSERRGWDQYLFKNRPTDG--PPNSFYRSLYPK
                                                                                                                                                                                                                                                    DNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHD
                                                                                                                                                                                                      CLKVLTGHTGSVLCLQYDERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNG
                                                                                                                     LMVTCSKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTS
                                                                                                                                                                                      TCEFVRTLNGHKRGIACLOYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chiaur, D.
APPLICANT: Pagano, M.
APPLICANT: LALES, E.
TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS
PILE REFERENCE: 5914-081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31;
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                                                                                                                                                                                                                                                                                                                                           DIILIWDFLNVPPSAQNETRSPSRTYTYISR 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/385,219A
CURRENT FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: 60/098,355
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-02-03
PRIOR PILING DATE: 1999-02-03
PRIOR PILING DATE: 1999-02-03
PRIOR PILING DATE: 1999-02-03
PRIOR PILING DATE: 1999-03-15
NUMBER OF SEQ ID NOS: 90
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Best Local Similarity 79.0%
Matches 451; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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                                                                                                                                                                                                                                                           STLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFLNVPPSAQNETRSPSRTYTYI 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Manning, Anthony M.
APPLICANT: Manning, Anthony M.
APPLICANT: Maccurio, Frank
APPLICANT: Amercurio, Frank
APPLICANT: Amercurio, Frank
APPLICANT: Ben-Neriah, Yinon
APPLICANT: Davis, Matti
APPLICANT: Davis, Matti
APPLICANT: Arcubal, Ada
APPLICANT: Yaron, Avraham
APPLICANT: Yaron, Avraham
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
TITLE OF INVENTION: NF-KB
FILE REFERENCE: 860098.427
CURRENT APPLICATION NUMBER: US/09/832,161
CURRENT FILING DATE: 2001-04-09
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEC ID NOS: 30
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        361 GHRAAVNVVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQYRDRLVVSGS
                                                                                                                                                                                                            421 SDNTIRLWDIECGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPA
                                                                                                                                                                                                                                                                            STLCLRTLVEHSGRVFRLQFDEFQIISSSHDDTILIWDFLNVPPSAQNETRSPSRTYTYI
                                                          TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLV
                                                                                                                          GHRAAVNVVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQYRDRLVVSGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        82.8%; Score 2384.5; DB 2
79.0%; Pred. No. 6.4e-227;
iive 48; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18, Application US/09832161; Patent No. 6656713; GENERAL INFORMATION:
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Best Local Similarity 79.09
Matches 451; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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US-09-832-161-18
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359 MMVTCSKDRSIAVWDWASPIDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRIIKVWNTS 418
                                                                                                                                                                                                                                                                                                                               419 TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF
                                                                        272 CLKVLTGHTGSVLCLQYDERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNG
                                                                                                                                                     LMVTCSKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTS
                                                                                                                                                                                                                                                                                                           DNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHD
212 IIQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISGLRDNSIKIWDKTSLB
                                                                                                                                                                                                                                  TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30. Application US/08190802A
; Sequence 30. Application US/08190802A
; Patent No. 5519003
; GENERAL INFORMATION:
    APPLICANT: Mochly-Rosen, Daria
    APPLICANT: Ron, Dorit
; TITLE OF INVENTION: Who-40 - Derived Peptides and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: P.O. Box 60850
; CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33.875
REGISTRATION NUMBER: 33.875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 2286.5; DB 1;
Pred. No. 2.8e-217;
                                                                                                                                                                                                                                                                                                                                                                                       512 DTILIWDFLNVPPSAQNETRSPSRTYTYISR 542
                                                                                                                                                                                                                                                                                                                                                                                                                          539 DTILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 8600-0139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 30: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79.4%;
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Best Local Similarity
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US-08-190-802A-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WORVISEGMLWKKLIERMVRTDPLWKGLSERRGWDQYLFKNRPTDG--PPNSFYRSLYPK 211
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                      299 CKRILTGHTGSVLCLQYDERVIITGSSDSTVRVWDVNTGEMLNTLIHHCEAVLHLRFNNG
                                                                                                 TCEFVRTLNGHKRGIACLOYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF
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                                                                          LMVTCSKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTS
                                                                                                                                                     TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31;
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                                                                                                                                                                                                                                                                                                             542
                                                                                                                                                                                                                                                                                                                                       APPLICANT: BENAROUS, Richard
APPLICANT: DENAROUS, Richard
APPLICANT: MARGOTTIN, Florence
APPLICANT: MARGOTTIN, Florence
APPLICANT: ARENZANA SEISDEDOS, Fernando
APPLICANT: CNURAND, Herve
APPLICANT: CONDORCET, Jean-Paul
TITLE OF INVENTION: Human beta-TrCP protein
FILE REFERENCE: 935.38812X00
CURRENT APPLICATION NUMBER: US/09/601,168B
CURRENT FILING DATE: 1999-01-29
PRIOR PILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: FR98 01100
PRIOR FILING DATE: 1999-01-30
PRIOR PILING DATE: 1999-01-30
PRIOR PILING DATE: 1998-12-09
                                                                                                                                                                                                                                                                                                             DIILIWDFLNVPPSAQNETRSPSRTYTYISR
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Patent No. 6730486
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                                                                                                                                                                                                                                                                                                                                                                                         94 HGHINTYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCSAELVCKEWYRVTSDGML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  274 SVLCLQYDERVIITG-SDSTVRVWDVNTGEMLATLIHHCEAVLHLRFNNGMVTCSKDRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 SVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 NWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISGLRDNSIKIWDKTSLECLKVLTGHTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 NWRCGRHSLQRIHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKNTLECKRVLMGHTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 SVLCLQYDERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  342 IAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLNG
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                                                                                                                                                                                                                                                                                                                                                                          104 HGHINSYLKPMLORDFITALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGML
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Sequence 30, Application US/08473089
Sequence 30, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
ITILE OF INVENTION: Thereof
ITILE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Poerster
                                                                                                                                                                                                                                   Query Match 79.4%; Score 2286.5; DB 2; Best Local Similarity 87.8%; Pred. No. 2.8e-217; Matches 423; Conservative 33; Mismatches 23;
                                                                                                                                                                                     BETA TRCP, Fig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 2000 Pennsylvania Avenue,
CITY: Washington
STATE: DC
ZIP: USA
ZIP: 20006-1812
        TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
                                     TOPOLOGY: ....ERISTICS:
TOPOLOGY: ....t
(202) 887-1500
                                                                                                              MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
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                                                                                                                                                                                     INDIVIDUAL ISOLATE:
                                                                                                                                                                      ORIGINAL SOURCE
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                                                                                                     HGHINSYLKPMLQRDFITALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGML 163
                                                                                                                     94 HGHINTYLKPMLQRDFITALPARGLDHIAENILSYLDAKSLCSAELVCKEWYRVTSDGML 153
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                                                       34 TLRQTKLANGTSSMIVPKQRKLSANYEKEKELCVKYFEQWSECDQVEFVEHLISRMCHYQ 93
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   23; Indels
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APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-40N-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/487,072
FILING DATE: 07-50N-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.

REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
   Mismatches
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2000 Pennsylvania Avenue, NW
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6262023
GENERAL INFORMATION:
   33;
   Conservative
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US-08-477-346-30
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Mochly-Rosen, Daria
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURACHIGE, KATE H.
REGISTRATION NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-1063
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
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INDIVIDUAL ISOLATE: BETA TRCP, Fig. 13
US-08-473-089-30
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                                                                                                                                                                                                                                                              TYPE: amino acids
TYPE: amino acids
TOPOLOGY: """
OIROTTE
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Best Local Similarity 87.8%;
Matches 423; Conservative
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US-08-487-072A-30
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44 SVRCLQISNGTSSVIVSRKRPSEGNYQKEKDLCIKYPDQWSESDQVEFVEHLISRMCHYQ 103
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APPLICANT: Non, Dorit, waita
APPLICANT: Ron, Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dorit Dor
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COMPUTRY: USA
ZIP: 20066-1812
ZIP: 20066-1812
COMPUTER READABLE FORM:
MEDIUT TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-UN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H:
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEFAX: (202) 887-1500
TELEFAX: (202) 887-1500
TELEFAX: (202) 887-1500
TELEFAX: 517 Amino acids
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87.8%; Pred. No. 2.8e-217;
tive 33; Mismatches 23;
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US-08-487-072A-30
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Matches 423; Conservative
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RESULT 11
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48 LOISNGTSSVIVSRKR----PSEGNYQKEKDLCIKYFDQWSESDQVBFVEHLISRMCHY
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Matches 163; Conservative 101; Mismatches 210;
                                                                                                                                                          APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and
TITLE OF INVENTION: Encode Them
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                                                                                                                                                                                                                              FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 21
LENGTH: 626
                                                                                                                     Sequence 21, Application US/09213888A
Patent No. 6638731
                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                               GENERAL INFORMATION:
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                                            GENERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Gurney, Adele M.
APPLICANT: Di, Jinh Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION UNMER: US/09/328,877D
CURRENT APPLICATION OFFER: 1999-06-09
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Ratentin Ver. 2.0
SSOTUD NO 21
LENGTH: 626
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22.3%; Score 643; DB 2; Length 62
Best Local Similarity 30.2%; Pred. No. 1.9e-54;
Matches 163; Conservative 101; Mismatches 210; Indels
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Sequence 21, Application US/09328877D Patent No. 6730778
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APPLICANT: Gurney, Mark E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; CTHER INFORMATION: Description
; OTHER INFORMATION: homo sapien
US-09-328-877D-21
                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Query Match
Best Local Similarity
JS-09-213-888-10
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              APPLICANT: Pauley, Adele M.
APPLICANT: Pauley, Adele M.
APPLICANT: Pharmacia & Upjohn Company
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
CURRENT FILING DATE: 1998-12-17
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Gurney, Mark E.
APPLICANT: Danley, Adele M.
APPLICANT: Pauley, Adele M.
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynuclectides that
TITLE OF INVENTION: Encode Them
FILE REFERENCE: 6142
CURRENT APPLICATION NUMBER: US/09/213,888A
WUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                             h 22.3%; Score 641.5; DB 2; Length 540; Similarity 32.1%; Pred. No. 2.1e-54; 43; Conservative 89; Mismatches 177; Indels 37
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; Patent No. 6638731
                                                                                                                                                                                                                                                    ; ORGANISM: Homo sapiens
US-09-213-888-7
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LENGTH: 540
TYPE: PRT
ORGANISM: Homo sapiens
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US-09-213-888-10
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APPLICANT: Gurney, Mark E.

APPLICANT: Janhe

APPLICANT: Fauley, Adele M.

APPLICANT: Pauley, Adele M.

APPLICANT: Pauley, Adele M.

APPLICANT: Pauley, Adele M.

APPLICANT: Pharmacia & Upjohn Company

TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that

TITLE OF INVENTION: Encode Them

FILE REFERENCE: 612

CURRENT APPLICATION NUMBER: US/09/328,877D

CURRENT FILING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 32

SOFTWARE: PatentIn Ver. 2.0
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      Length 540;
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22.3%; Score 641.5; DB 2; Length 32.1%; Pred. No. 2.1e-54; ive 89; Mismatches 177; Indels
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      Query Match 22.3
Best Local Similarity 32.1
Matches 143; Conservative
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US-09-328-877D-7
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SYLDARSICAAELVCKEWQRVISEGMLWKKLIERMVRTDPLWKGLSERRGWDQYL-FKNR 195
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                                     LRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLV---EHS 492
                                                                             ----OCLOTLOGPNKHQ 457
347 VVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNC 406
                                                                                                                                                                                                                                       US-09-213-888-6

Sequence 6, Application US/09213888A

Sequence 6 Application US/09213888A

Patent No. 663871

GENERAL INFORMATION:

APPLICANT: Gurney, Mark E.

APPLICANT: Di, Jinhe

APPLICANT: Dauley, Adele M.

APPLICANT: Pauley, Adele M.

TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that

TITLE OF INVENTION: Encode Them

TITLE OF INVENTION: Encode Them

CURRENT APPLICATION NUMBER: US/09/213,888A

CURRENT APPLICATION NUMBER: US/09/213,888A

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 6:

SEQ ID NO 6:
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                                                                               407 IHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTG---
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; Pred. No. 2.1e-54;
89; Mismatches 177;
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Best Local Similarity 32.1%;
Matches 143; Conservative 89
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US-09-213-888-6
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          PTDGPPNSFYRSLYPKIIQDIETIESNWRCGRHNLORIQCRSENSKGVYCLQYDDEKIIS
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Patent No. 6730778

GRNERAL INFORMATION:
APPLICANT: Gurney, Mark E.
APPLICANT: Li, Jinhe
APPLICANT: Pauley, Adele M.
APPLICANT: Pauley, Adele M.
APPLICANT: Pauley, Adele M.
TITLE OF INVENTION: Human Sel-10 Polypeptides and Polynucleotides that
TITLE OF INVENTION: Encode Them
FILE REPERBUCE: 6142
CURRENT APPLICATION NUMBER: US/09/328,877D
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 32
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Matches 143; Conservative
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ORGANISM: Homo sapiens
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US-09-328-877A-7
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US-10-653-496A-7
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## ALIGNMENTS

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US-09-832-161-16
; Sequence 16, Application US/09832161
; Publication No. US20030166587A1
; Publication No. US20030166587A1
; GENERAL INFORMATION:
; APPLICANT: Manning, Anthony M.
APPLICANT: Marcurio, Frank
; APPLICANT: Amit, Sharon
; APPLICANT: Davis, Matti
APPLICANT: Lavon, Iris
APPLICANT: Lavon, Iris
APPLICANT: Lavon, Iris
; APPLICANT: Harzubai, Ada
; APPLICANT: Harzubai, Ada
; APPLICANT: Harzubai, Ada
; APPLICANT: Harzubai, Ada
; APPLICANT: Waron Nowellan
; TITLE OF INVENTION: OCMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF
TITLE OF INVENTION: NP-MB
; TITLE OF INVENTION: NP-MB
; TILLE REFERENCE: 860098-427
; CURRENT APPLICATION NUMBER: 09/210,060
; PRIOR FILING DATE: 200-04-09
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin Ver. 2.0
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.larity 100.0%; Pred. No. 1.3e-244;
Conservative 0; Mismatches 0;
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ORGANISM: Homo sapiens
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Db   241 KGVYCLQYDDEKIISGLRDNSIKIMDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS 300	RESULT 3  US-09-832-161-18  Squence 18, Application US/09832161  SQUENCE 18, Application US/09832161  SQUENCE 18, Application No. US20030166587A1  GENERAL INFORMATION:  APPLICANT: Menting, Anthony M.  APPLICANT: Amit, Sharon  APPLICANT: Davis, Matti  APPLICANT: Hatzubai, Ada  A	Query Match 82.8%; Score 2384.5; DB 3; Length 569; Best Local Similarity 79.0%; Pred. No. 5.3e-201; Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps	Qy 1 MEP-DSVIEDKTIELMCSVPRSLWLGCANLVESMCAL		OY 94 HLISRMCHYQHGHINSYLKPMLQRDFITALPEQGLDHIAENILSYLDARSLCAAELVCKE 153	Qy 154 WQRVISEGMLWKKLIERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPK	QY 212 IIQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIISGLRDNSIKIWDKTSLE
Db 241 KGVYCLQYDDEKIISGLRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDERVIVTGSSDS 300  Qy 301 TVRVWDVNTGEVLNTLIHHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLV 360  L	RESULT 2 US-10-665-715-16 Sequence 16, Application US/10665715 Sequence 16, Application US/10665715 Sequence 16, Application US/10665715 Sequence 16, Application No. US20040203098A1 GENERAL INFORMATION: APPLICANT: Manning, Anthony M. APPLICANT: Marcurio, Frank APPLICANT: Ben-Neriah, Yinon APPLICANT: Ben-Neriah, Yinon APPLICANT: Lavon, Iris AP	Query Match 100.0%; Score 2879; DB 4; Length 542; Best Local Similarity 100.0%; Pred. No. 1.3e-244; Matches 542; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Qy 1 MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLQSMPSVRCLQISNGTSSVIVS 60 1 MEPDSVIEDKTIELMCSVPRSLWLGCANLVESMCALSCLQSMPSVRCLQISNGTSSVIVS 60	Qy         61 RKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFI 120           Db         61 RKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVEHLISRMCHYQHGHINSYLKPMLQRDFI 120	Qy         121 TALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLIERWYRTDFLWKG 180           Db         121 TALPEQGLDHIAENILSYLDARSLCAAELVCKEWQRVISEGMLWKKLIERWYRTDFLWKG 180	Qy 181 LSERRGWDQYLFKNRPTDGPPNSFYRSLYPKIIQDIETIESNWRCGRHNLQRIQCRSENS 240  181 LSERRGWDQYLFKNRPTDGPPNSFYRSLYPKIIQDIETIESNWRCGRHNLQRIQCRSENS 240	Qy 241 KGVYCLQYDDEKIISGLRDNSIKIWDKTSLECLKVL7GHTGSVLCLQYDERVIVTGSSDS 300

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61 S--TAMKTENCVAKTKLANGTSSMIVPKQRKLSASYEKEKELCVKYFEQWSESDQVEFVE 118
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Sequence 8, Application US/10038010
| Sequence 8, Application US/10038010
| Publication No. US20030040089A1
| GENERAL INFORMATION:
| APPLICANT: HYBRIGENICS
| APPLICANT: Pierre, Legrain
| TITLE OF INVERTION: Protein-protein interactions in adipocyte cells
| FILE REFERENCE: B476A7
| CURRENT APPLICATION NUMBER: US/10/038,010
| CURRENT PILING DATE: 2002-07-23
| PRIOR APPLICATION NUMBER: US 60/259,377
| PRIOR APPLICATION NUMBER: US 60/259,377
| SOFTWARE: Patentin version 3.1
| SEQ ID NO 8
| LENGTH: 569
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Best Local Similarity 79.0°
Matches 451; Conservative
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Selection US/20020123082A1
Subjection No. US20020123082A1
Subjection No. US20020123082A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
M. TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF FILE REPERENCE: 5914-090-942,417
CURRENT FILING DATE: 2002-01-07
PRIOR PELLOR FULLING DATE: 2001-01-5
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 2
SEQ ID NO 2
LENGTH: 569
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                           LMVTCSKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTS
                                                                                            TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF
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Best Local Similarity 79.09
Matches 451; Conservative
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                   TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF
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GENERAL INFORMATION.

APPLICANT: Pagano, M.

APPLICANT: Pagano, M.

APPLICANT: Latries, B.

TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS

FILE REFERENCE: 5914-081

CURRENT APPLICATION NUMBER: US/10/652,928

CURRENT FILING DATE: 1209-08-28

PRIOR APPLICATION NUMBER: US/09/385,219A

PRIOR APPLICATION NUMBER: G0/098,355

PRIOR PILING DATE: 1998-08-28

PRIOR FILING DATE: 1998-08-28

PRIOR FILING DATE: 1999-03-18

PRIOR FILING DATE: 1999-03-15

PRIOR SPLING DATE: 1999-03-15

NUMBER OF SEQ ID NOS: 90

SOFTWARE: PALENTIN VEY: 2.0

SEQ ID NO 2

SEX ID NO 2

CHARACTER APPLICATION NUMBER: G0/124,449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
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Best Local Similarity 79.0%; Pred. No. 5.3e-201;
Matches 451; Conservative 48; Mismatches 41;
                                                                                                              DILLIWDFLNVPPSAQNETRSPSRTYTYISR 542
                                                                                                                                  ; Sequence 2, Application US/10652928
; Publication No. US20050079558A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MEP-DSVIEDKTIELMCS-
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US-10-085-/15-18-18

Sequence 18, Application US/10665715

Publication No. US20040203098A1

GENERAL INFORMATION:

APPLICANT: Manchio, Frank

APPLICANT: Marcurio, Frank

APPLICANT: Marcurio, Frank

APPLICANT: Bavis, Matti

APPLICANT: Bavis, Matti

APPLICANT: Hatubai, Ada

APPLICANT: Hatubai, Ada

APPLICANT: Hatubai, Ada

APPLICANT: Lavon, Iris

APPLICANT: Lavon, Iris

APPLICANT: Varon, Avraham

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING ACTIVATION OF

TITLE OF INVENTION: NP-kB

FILE REFERENCE: 860098-427

CURRENT APPLICATION NUMBER: US/09/210,060

PRIOR APPLICATION NUMBER: US/09/210,060

PRIOR FILING DATE: 1998-12-10

NUMBER OF SEQ ID NOS: 30

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 18

LENGTH: 569

TYPE: PRT

ORGANISM: Homo sapiens

US-10-665-715-18
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                                                                                                                                     Query Match
Best Local Similarity
Matches 451; Conserv
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Sequence 2, Application US/11073485
; Sequence 2, Application US/11073485
; Dublication No. US20050208601A1
; GENERAL INFORMATION:
    APPLICANT: Pagano, N.
    TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLI
    TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
    FILE REFERENCE: 5914-090-999
; CURRENT APPLICATION NUMBER: US/11/073,485
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/042,417
; PRIOR APPLICATION NUMBER: 60/260,179
; PRIOR FILING DATE: 2001-01-07
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2.
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                                                                                                                                          1 MEP-DSVIEDKTIELMCS-----
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Matches 451; Conservative
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ORGANISM: Homo sapiens
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US-11-073-485-2
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Sequence 2, Application US/10632150

Publication No. US20050251871A1

GENERAL INFORMATION:

APPLICANT: Chiaur, D.

APPLICANT: Dagano, M.

APPLICANT: Latres, E.

TITLE OF INVENTION: NOVEL UBIQUITIN LIGASES AS THERAPEUTIC TARGETS

FILE REFERENCE: 5914-081

CURRENT APPLICATION NUMBER: US/10/632,150

CURRENT APPLICATION NUMBER: US/99385,219

PRIOR APPLICATION NUMBER: G0/098,355

PRIOR FILING DATE: 1999-08-28

PRIOR FILING DATE: 1999-03-15

PRIOR APPLICATION NUMBER: 60/118,568

PRIOR FILING DATE: 1999-03-3

PRIOR FILING DATE: 1999-03-3

PRIOR FILING DATE: 1999-03-15

NUMBER OF SEQ ID NOS: 90

SOFTWARE: PATENTIN VET. 2.0

SEQ ID NO 2

LENGTH: 66-9
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82.8%; Score 2384.5; DB 5;
Best Local Similarity 79.0%; Pred. No. 5.3e-201;
Matches 451; Conservative 48; Mismatches 41; I.
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US-10-632-150-2
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us-10-665-715-16.rapbm

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TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIFE TITLE OF INVENTION: AND DIFFERENTIATIVE DISORDERS
FILE REFERENCE: 5914-090-999
FILE REFERENCE: 5914-090-999
FILE REFERENCE: 5014-090-999
FILE REFERENCE: 5014-090-999
PRIOR APPLICATION NUMBER: US/11/073,457
CURRENT FILING DATE: 2005-03-04
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR APPLICATION NUMBER: 60/260,179
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 92
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
LENGTH: 569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF 451
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; Pred. No. 5.3e-201;
48; Mismatches 41;
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DTILIWDFLNDPAAQAEPPRSPSRTYTYISR 569
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                                                                                                                                                                                                                                                                                                                                                       82.8%;
                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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US-11-073-457-2
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Best Local Simil
Matches 451; (
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US-11-099-691-12
                                          RESULT 11
US-11-073-457-2
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TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEF
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEF
FILE REPERENCE: $914-090-999
CURRENT PAPLICATION NUMBER: US/11/073,470
CURRENT FILING DATE: $2005-03-04
PRIOR APPLICATION NUMBER: 10/042,417
PRIOR PILING DATE: $2005-01-07
PRIOR PILING DATE: $2005-01-05
NUMBER OF $80 ID NOS: 92
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: $69
TYPE: PRI
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                                                               DTILIWDFLNVPPSAQNETRSPSRTYTYISR 542
                                           DTILIMDFLNVPPSAQNETRSPSRTYTYISR
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; Publication No. US20050214879A1
; GENERAL INFORMATION:
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US-11-073-470-2
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US-11-073-470-2
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Best Local Similarity 79.0
Matches 451; Conservative
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79.0%; Pred. No. 5.3e-201;
tive 48; Mismatches 41; Indels 31;
                                 GENERAL INCOMPATION:
APPLICANT: INCYTE PHARMACEUTICALS, INC.
APPLICANT: HILLMAN, OGENIÉE L.
APPLICANT: HILLMAN, OGENIÉE L.
APPLICANT: HILLMAN, OGENIÉE L.
APPLICANT: HILLMAN, JORNIÉE L.
APPLICANT: YUE, HENTY
APPLICANT: TAME, Y'COM
APPLICANT: PATTERSON, Chandra
APPLICANT: PATTERSON, Chandra
APPLICANT: PATTERSON, CHANGER
APPLICANT: PATTERSON, CHANGER
APPLICANT: PATTERSON, CHANGER
TITLE OF INVENTION: CELL SIGNALING PROTEINS
FILE REFERENCE: PF-0521 PCT
CURRENT FILING DATE: 2005-04-06
PRIOR APPLICATION NUMBER: US/09/700,444
PRIOR APPLICATION NUMBER: 60/085,343
PRIOR PILING DATE: 1998-06-13
PRIOR PILING DATE: 1998-06-13
PRIOR FILING DATE: 1998-08-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PRIL
TYPE: PRIL
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc-feature
OTHER INFORMATION: Incyte Clone 3239149
Application US/11099691
             Publication No. US20050260644A1
GENERAL INFORMATION:
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Matches 451; Conservative
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Sequence 2, Application US/11073460

Sequence 2, Application US/11073460

Publication No. US20050272066A1

GENERAL INFORMATION:

TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF

TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF

TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT OF PROLIF

TITLE OF INVENTION: MUMBER: US/11/073,460

CURRENT APPLICATION NUMBER: US/11/073,460

PRIOR PRILING DATE: 2005-01-07

PRIOR FILING DATE: 2005-01-07

PRIOR FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 92

SOFTWARE: PATCHTIN Ver. 2.0
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                                                                     APPLICANT: Orlicky, Stephen
APPLICANT: Sicheri, Frank
APPLICANT: Sicheri, Frank
APPLICANT: Tyers, Mike
APPLICANT: Willems, Andrew
APPLICANT: Tang, XiaoJing
TITLE OF INVENTION: Structures of Substrate Binding Pockets of SCF Complexes
FILE REFERENCE: 14096.340511
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: US 60/419,606
PRIOR APPLICATION NUMBER: US 60/419,606
PRIOR PLING DATE: 2003-10-17
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PetentIn version 3.2
SEQ ID NO 18
LENGTH: 569
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DTILIWDFLNDPAAHAEPPRSPSRTYTYISR 569
                                                                                                                                                                                                                                                                                                                         ORGANISM: Mus musculus
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank/NP_033901
DATABASE ENTRY DATE: 1998-08-04
RELEVANT RESIDUES: (1)..(569)
                         ; Sequence 18, Application US/10687732; Publication No. US20040171074A1; GENERAL INFORMATION:
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Best Local Similarity 78.6
Matches 449; Conservative
RESULT 14
US-10-687-732-18
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                                                                                                                                                                                               NUCLEIC ACID
EXPRESSION OF 10,000 OR MORE
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80.8%; Pred. No. 5.2e-174;
ive 44; Mismatches 46; Indels 1;
                                                                                                                             GEMERAL INFORMATION:
GEMERAL INFORMATION:
APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCTITLE OF INVENTION: DENOSPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLOOD'28
CURRENT FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/167,832
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-22
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PRIOR FILING DATE: 2000-01-12
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PRIOR FILING DATE: 2000-01-28
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PRIOR FILING DATE: 2000-01-3
RESULT 15
US-11-097-143-6363
Sequence 6363, Application US/11097143
Publication No. US20050208558A1
GENERAL INFORMATION:
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Best Local Similarity 80.81
Matches 384; Conservative
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US-11-097-143-6363
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Search completed: August 25, 2006, 07:38:23 Job time : 187 secs

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Sequence 6, Application US/10968871

Sequence 6, Application US/10968871

Sequence 6, Application OS US2006017782941

GENERAL INFORMATION:

APPLICANT: New York University

APPLICANT: New York University

APPLICANT: New York University

TITLE OF INVENTION: Methods to Identify Compounds Useful For Tumor Sensitization to

TITLE OF INVENTION: DNA Damage

FILE REFERENCE: 05986/0200145-US0

CURRENT APPLICATION UNDABER: US/10/968,871

CURRENT FILING DATE: 2004-10-18

NUMBER OF SEQ ID NOS: 29

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542; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 542; Conserv
                                                                                                                                                                                                                                                                                                                              LENGTH: 542
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Qy         452 DNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHD         511           Db         479 DNKRIVSGAYDGKIKVWDLVAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHD         538           Qy         512 DTILIMDFLNVPPSAQNETRSPSRTYTYISR         542           Db         539 DTILIMDFLNDPAAQAEPPRSPSRTYTYISR         569           RESULT         3           "	APPLICANT: Latres, Esther APPLICANT: Latres, Esther APPLICANT: Chandawarker, Rajiv TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT TITLE OF INVENTION: OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS FILE REFERENCE: 5914-106-999 CURRENT APPLICATION NUMBER: US/11/106,014 CURRENT FILING DATE: 2003-07-30 PRIOR APPLICATION NUMBER: 10/612,150 PRIOR PELING DATE: 2002-01-07 PRIOR APPLICATION NUMBER: 09/385,219 PRIOR FILING DATE: 1999-08-27 PRIOR PELING DATE: 1999-02-03 PRIOR PELING DATE: 1999-02-03 PRIOR PELING DATE: 1999-02-03 PRIOR PELING DATE: 1999-02-03 PRIOR PELING DATE: 1999-02-03 PRIOR PELING DATE: 1998-02-03 PRIOR PELING DATE: 1999-02-03 PRIOR PELING DATE: 1999-02-03 PRIOR PELING DATE: 1999-02-03 PRIOR PELING DATE: 1999-02-03 PRIOR PELING DATE: 1999-03-03	; NUMBER OF SEQ ID NOS: 96 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 2 ; TENGTH: 569 ; TYPE: RT ; ORGANISM: Homo sapiens US-11-106-014-2	Query Match Best Local Similarity 79.0%; Pred. No. 2e-184; Matches 451; Conservative 48; Mismatches 41; Indels 31; Gaps 7;  Qy 1 MEP-DSVIEDKTIELMCSVPRSLWLGCANLVESMCAL 36		119	
Qy         361 GHRAAUNUVDFDDKYIVSASGDRTIKUWSTSTCEFURTLNGHKRGIACLQYRDRLVVSGS 420           Db         361 [	RESULT 2  US-10-566-871-3  Sequence 3, Application US/10968871  Sequence 3, Application US/10968871  Sequence 3, Application US/10968871  Sequence 3, Application OS US2006017782941  GENERAL INFORMATION:  APPLICANT: Pagano, Michele  TITLE OF INVENTION: Methods to Identify Compounds Useful For Tumor Sensitization to TITLE OF INVENTION: DNA Damage  FILE REFERENCE: 05986/0200145-USO  TITLE OF INVENTION: UNMBER: US/10/968,871  CURRENT FILING DATE: 2004-10-18  NUMBER OF SEQ ID NOS: 29  SOFTWARE: Patentin Version 3.2  SEQ ID NO 3  LENGTH: S69  TYPE: PRT  ORGANISM: Home sapiens  US-10-568-871-3	82.8%; Score 2384.5; DB 6; Length 569; 79.0%; Pred. No. 2e-184; ive 48; Mismatches 41; Indels 31; Gaps IELMCS	Db 1 MDPAEAVLQEKALKFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCLNQETVCLA 60  Qy 37 SCLQSMPSVRCLOISNGTSSVIVSRKRPSEGNYQKEKDLCIKYFDQWSESDQVEFVE 93	119 HIISQMCHYQHGHINSYLKPMLQRDFITALPARGLDHIABNILSYLDAKSLCAAELVCKE 154 WQRVISEGMLWKKLIERMVRTDPLWKGLSERRGWDQYLFKNRPTDGPPNSFYRSLYPK	Qy         212 IIQDIETIESNWRCGRHNLQRIOCRSBNSKGYCLQYDDEKIISGLRONSIKTWDKTSLE 271           Db         239 IIQDIETIESNWRCGRHSLQRIHCRSETSKGYCLQYDDKIIS[	Qy         332 LMVTCSKDRSIAVWDMASATDITLERRULVGHRAAVNVVDFDDKYIVSASGDRTIKVWSTS 391           bb         :

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Query Match
Best Local Similarity
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                                                                                                                     511
                                                                                                                                   249 DDEKIISGLRDNSIKIWDKTSLECLKVLTGHTGSV--LCLQYDERVIVTGSSDSTVRVWD 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          923 IDQTLRVWDVSSSLSPSSSSSGGAGLRERQGHTKDVNSVAFPPDGKRLASGSDDQSVRV 982
                                                  451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      806 TATGETLRELKGHTGWVRSVAFSTDGQRIVTGGDDQSVRVWDASTGECV---RELKGYTA 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        863 ALISVAFSPDGQRIVSGGGDQTVRVWNAATGECQCELKGHTEQVDSIAFSPDGQHIVSGS 922
                                                                                                                                                                                                                                                                                                Sequence 42312, Application US/10449902

Sequence 42312, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: Bio-oriented Fechnology Research Advancement Institution.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REPERENCE: MOA-A02051-US

CURRENT FILING DATE: 2003-05-29

FRIOR PLING DATE: 2003-05-39

PRIOR FILING DATE: 2002-05-30

PRIOR PLING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: Patentin Ver. 2.1
419 TCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEELVRCIRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          365 AVNVVDF--DDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQYR--DRLVVSGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           421 SDNTIRLWDIEC-----GACLRVLEGHEELVRCIRF--DNKRIVSGAYDGKIKV
                                                                                                                     DNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQFDEFQIISSSHD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35;
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                                                                                                                                                                                        DIILIWDFLNVPPSAQNETRSPSRTYTYISR 542
                                                                                                                                                                                                        Sequence 4324, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
A PAPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 35.8
Matches 105; Conservative
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US-10-449-902-42332
                                                                                                                                                                                                                                                                                          -10-449-902-42332
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ORGANISM:
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44 LVEEIQKAEPLLTASRTEQVKLLIQRLQEKLGQNSNHTFYLFKVLKAHILPLTNVALNKS 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 -EKIISGLRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYDER--VIVTGSSDSTVRVWDV 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    308 NTGEVLNTLIHHNEAVLHLRF--SNGLMVTCSKDRSIAVWDMASATDITLRRVLVGHRAA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNVVDF--DDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGI--ACLQYRDRLVVSGSS 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :: | | | :: | | :: | |: | |: | 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNTIRLWDIECGACLRVLEGHEELVRCIRFD--NKRIVSGAYDGKIKVWDLQAALDPRAP 479
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APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
TITLE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 90488
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    78;
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                                                                                                                                                                                                                                                                                                                                               Length 415;
                                                                                                                                                                                                                                                                                                                                               13.7%; Score 395; DB 7; Length 41
25.8%; Pred. No. 4.5e-24;
tive 79; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480 ASTLCLRTLVEHSGRVFRLQFDEFQ--IISSSHDDTILIW 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            --KGLSERRGWDQ----YLFK-
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Pred. No. 6.1e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 GSCFITGSYDRTCKLWDTASGEELNTLE-----GHRNV-
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; OTHER INFORMATION: Ceres Seq. ID no. 12724103
US-11-056-3558-90488
                   CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 4324
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ORGANISM: Arabidopsis thaliana
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31.0%;
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FILE REFERENCE: H1-A0106
                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Homo sapiens
US-11-293-697-4324
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Best Local Similarity
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ORGANISM: Homo sapiens
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7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFSVTNGKRIVSGSEDNCVHMWELNSKKLLQKLEGHTETVMNVACHPTEN-LIASGSLDK 307
                                                 GSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFS--NGLMVTCSKDRSIAVWDMASATDI 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ----YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEEL---VRCIRFDNKRIVSGAYDG 463
                                                                                                                                                354 TLRRVLVGHRAAVNVVDF--DDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQ- 410
                                                                                                                                                                                                         ----YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEEL---VRCIRFDNKRIVSGAYDG 463
                                                                                                                                                                                                                          296 GSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFS--NGLMVTCSKDRSIAVWDMASATDI 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            189 CVKTLIDDENPPVSFVRFSPNGKFILVGTLDNTLRLWNISSAKFLKTYTGHVNAQYCISS
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
TITLE OF INVENTION: Polypeptides Encoded Thereby
CURRENT APPLICATION NUMBER: US/11/056,3558
CURRENT APPLICATION NUMBER: 105/11/056,3558
CURRENT PILING DATE: 2005-02-14
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238 ENSKGVYCLQYDDEKIISGLRDNSIKIWDKTSLECLKVLTGHTGSVLCLQYD--ERVIVT
                             238 ENSKGVYCLOYDDEKIISGLRDNSIKIWDKTSLECLKVLTGHTGSVLCLOYD--ERVIVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 7; Length 317;
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 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.4%; Score 329.5; DB 7;
larity 31.0%; Pred. No. 6.1e-19;
Conservative 50; Mismatches 102;
 102;
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; OTHER INFORMATION: Ceres Seq. ID no. 12724103
US-11-056-355B-94244
   Mismatches
                                                                                                                                                                                                                                                                                                                                          RESULT 7
US-11-056-355B-94244
; Sequence 94244, Application US/11056355B
; Publication No. US20060150283A1
   20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: prt
ORGANISM: Arabidopsis thaliana
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nes 76; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVRIW 312
                                                                                                                                                                                                                                                                     464 KIKVW 468
                                                                                                                                                                                                                                                                                               308 TVRIW 312
                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 94244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 317
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APPLICANT: Stivastava, Promod
APPLICANT: Chandawarker, Rajiv
TITLE OF INVENTION: METHODS TO IDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT
TITLE OF INVENTION: OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
FILE REFERENCE: 5914-106-999
FILE REFERENCE: 5914-106-999
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Sequence 4, Application US/11106014
Publication No. US20060088846A1
GENERAL INFORMATION:
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APPLICANT: Chiaur, Dah Sharim
APPLICANT: Latres, Esther
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Best Local Similarity 22.5%
Matches 106; Conservative
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RESULT

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US-11-056-355B-85524
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Sequence 54504, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Poundation for Advancement of International Science.

ITLE REFERENCE: MOA-AQ205Y1-US

CURRENT FILING DATE: 2003-62-29

PRIOR PRILING DATE: 2003-05-29

PRIOR APPLICATION NUMBER: UP 2002-203269

PRIOR APPLICATION NUMBER: UP 2002-2383870

PRIOR FILING DATE: 2002-15-30

PRIOR PILING DATE: 2002-12-11

NUMBER OF SEQ ID NOS: 56791

SOFTWARE: PatentIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 37531, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
7 TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 DDEKIISGLRDNSIKIWDKTSLECLKVLTGHTGSVLCL----QYDERVIVTGSSDSTVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                354 TLRRVLVGHRAAVN--VVDFDDKYIVSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   618 WTIK-----TINECIATFDKHDGKVWALAVGKKTEMLATGGTDAVLNLW 660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.3%; Score 326; DB 6; Length 89
Best Local Similarity 27.4%; Pred. No. 4.7e-18;
Matches 80; Conservative 61; Mismatches 119; Indels
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LOCATION: (1)..(267)
OTHER INFORMATION: Ceres Seq. ID no. 12335591
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CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 37531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: prt
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-54504
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280 TGSVLCLQYD--ERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAV--LHLRFSNGLMVT 335
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                                                                                                                                                                                                                          CSKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDF--DDKYIVSASGDRTIKVWSTSTC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                180 KFLKVYTGHTNKVFCITSAFSVTNGKYIVSGSEDNCVYLWDLQARNILQRLEGHTDAVIS 239
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APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60,544,190
PRIOR FILING DATE: 2004-02-13
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                                                                                                                                            4 WSATNYSL--IHRYEGHSSGISDLAWSSDSHYTCSASDDCTLRIWDARSPYECLKVLRGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 WRCGRHNLQRIQCRSENSKGVYCLQY--DDEKIISGLRDNSIKIWD-KTSLECLKVLTGH
                                                                                                223 WRCGRHNLQRIQCRSENSKGVYCLQY--DDEKIISGLRDNSIKIWD-KTSLECLKVLTGH
                                              22;
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  Length 267;
                                              55; Mismatches 109;
, DB 7;
1.6e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: peptide
LOCATION: (1)..(267)
OTHER INFORMATION: Ceres Seq. ID no. 12680898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRCIRFDNKRIVSGAY-DGKIKVWDLQA 472
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11.2%; Score 323; 30.6%; Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: prt
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 85524
                                              Conservative
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                          Best Local Similarity
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, ORGANISM: Oryza sativa
US-10-449-902-50780
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LENGTH: 654
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Sequence 85523, Application US/11056355B

Publication No. US20060150283A1

GENERAL INPORMATION:

APPLICANT: Alexandrov, Nickolai

TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding

TITLE OF INVENTION: Polypeptides Encoded Thereby

FILE REPRENCE: 2750-1590PUS2

CURRENT APPLICATION NUMBER: US/11/056,355B

CURRENT FILING DATE: 2006-02-14

PRIOR FILING DATE: 2004-02-13

NUMBER OF SEQ ID NOS: 119966

SEQ ID NO 85523

LENGTH: 333
                                                                                 Sequence 37530, Application US/11056355B
; Publication No. US20060150283A1
; GENREAL INFORMATION:
    APPLICANT: Brover, Vyacheslav
; APPLICANT: Alexandrov, Nickolai
; TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
; TITLE OF INVENTION: Polypeptides Encoded Thereby
; FILE REFERENCE: 2750-1590PUS2.
; CURRENT APPLICATION NUMBER: US/11/056,355B
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,190
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 119966
; SEQ ID NO 37530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      223 WRCGRHNLQRIQCRSENSKGVYCLQY--DDEKIISGLRDNSIKIWD-KTSLECLKVLTGH 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 WSATNYSL--IHRYEGHSSGISDLAWSSDSHYTCSASDDCTLRIWDARSPYECLKVLRGH 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 TGSVLCLQYD--ERVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAV--LHLRFSNGLMVT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336 CSKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDF--DDKYIVSASGDRTIKVWSTSTC 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 ASHDGSCKIWDAKEGT--CLKTLIDDKSPAVSFAKFSPNGKFILVATLDSTLKLSNYATG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFVRTLNGHKRGIACLQ----YRDRLVVSGSSDNTIRLWDIECGACLRVLEGHEEL--- 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.2%; Score 323; DB 7; Length 33: 30.6%; Pred. No. 2.2e-18; tive 55; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           , LUCATION: (1)..(333)
; OTHER INFORMATION: Ceres Seq. ID no. 12335590
US-11-056-355B-37530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    446 VRCIRFDNKRIVSGAY-DGKIKVWDLQA 472
240 VSCHPVQNEISSSGNHLDKTIRIWKQDA 267
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ORGANISM: Arabidopsis thaliana
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                     TYPE: prt
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82; Conservative
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Best Local Similarity
                                                                           US-11-056-355B-37530
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US-11-056-355B-85523
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272 CLKVLTGHTGSVLCLQYDE--RVIVTGSSDSTVRVWDVNTGEVLNTLIHHNEAVLHLRFS 329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 WRCGRHNLQRIQCRSENSKGVYCLQY--DDEKIISGLRDNSIKIWD-KTSLECLKVLTGH 279
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT FILING DATE: 2003-60-29
CURRENT FILING DATE: 2003-60-29
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
                                                                                                                                                                                                                                                                   398 PYTLFQCHSGPVYSAAFSPFGDFLLSSSSDSTIRLW-----STKLNAN----
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                                                                                                                                                                                   22; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.2%; Score 323; DB 6; Length 654; 25.9%; Pred. No. 5.4e-18; Artive 55; Mismatches 103; Indels
                                                                                                                                                                                   Indels
                                                                                                                            Query Match
11.2%; Score 323; DB 7; L.
Best Local Similarity 30.6%; Pred. No. 2.2e-18;
Matches 82; Conservative 55; Mismatches 109;
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, LUCATION: (1)..(333)
; OTHER INFORMATION: Ceres Seq. ID no. 12680897
US-11-056-355B-85523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  446 VRCIRFDNKRIVSGAY-DGKIKVWDLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 50780, Application US/10449902
; Publication No. US20060123505A1
; GENERAL INFORMATION:
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Best Local Similarity 25.98
Matches 86; Conservative
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                                       448 CIRF--DNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVFRLQF--DEF 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          377 VSASGDRTIKVWSTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTIRLWDIECGACL 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                437 RVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLQAALDPRAPASTLCLRTLVEHSGRVF 496
                                                                                                                                                                                                                                                       Sequence 41350, Application US/10449902

Publication No. US20060123505A1

GENERAL INFORMATION:
APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
FILE REFERENCE: MOA-A0205Y1-US
CURRENT FILING DATE: 2002-203269
PRIOR APPLICATION NUMBER: UP 2002-203269
PRIOR APPLICATION NUMBER: UP 2002-383870
PRIOR APPLICATION NUMBER: UP 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 41350
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                                                                                                                          504 QIISSSHDDTILIWDFLNVPPSAQNETRSPSR 535
                                                                                                                                                    : | | | : : | : | 588 LLASGSADCTVKLWDVASSTKVLKTDDTSTNR 619
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; ORGANISM: Oryza sativa
US-10-449-902-41350
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